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Listing first 45 summaries
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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MYH7_RAT
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PROSITE; PS50096; IQ; 1.
MYOSin; Muscle protein; (
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InterPro; IPR002928; Myosin_tail.
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PF02736; myosin_N; 1.
PF01576; myosin_tail; 1.
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ALKYLATION (SH-1) (POTENTIAL).
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ALKYLATION (SH-2) (POTENTIAL).
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MEDLINE-95196755; PubMed-7889940;

MEDLINE-5 A Jordan M.A., Schaar B.T.,
                                                                                                                           Cell cycle; Centromere.
DOMAIN 1 335
DOMAIN 336 2471
DOMAIN 2472 2663
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EMBO J. 14:918-926(1995).
 1632 KMTAVN----
                                                                                                                                                                                    PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2;
                                                                                                                                                                                                          PRINTS; PR00380; KINESINHEAVY. SMART; SM00129; KISC; 1.
                                                                                                                                                                                                                                   Pfam; PF00225;
                                                                                                                                                                                                                                                        MIM; 117143;
                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                            entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mitosis
                                                                                                                                                                        Motor protein; Cell division; ATP-binding; Coiled
                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                          between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Mitotic HeLa cells contain a CENP-E-associated
microtubule motor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93024922; PubMed=1406971;
Yen T.J., Li G., Schaar B.T., Szilak I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       numu sapieus (numan).
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                             InterPro; IPR001752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Centromeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "CENP-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                       55 KRTIINKLFFDLAQEEENVLDREFLKNELDNVRAQLSQKDKEK-RDSQVIIDTLRDTLEE 113
                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: INTERACTS WITH CENP-F AND BUBRI KINASE.
SUBECLLULAR LOCATION: ASSOCIARIES WITH KINETOCHORES DURING
CONGRESSION, RELOCATES TO THE SPINDLE MIDZONE AT ANAPHASE,
QUANTITATIVELY DISCARDED AT THE END OF THE CELL DIVISION.
SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.
                                               93;
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                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is a putative kinetochore
                                                                                                                                                                                                                                                                                                                                                                       the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 39, protein E
                                               Conservative
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                                                                                                                                                                                                                                   kinesin;
                                                                                                      AΑ;
 -ETQEKMCEIEHLKEQFETQKLNLENIETENIRLTQI----LHENLEE 1680
                                                                                                      93
312087
                                                      7.9%;
25.1%;
                                                                                                                                                                                                                                             kinesin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last annotation update) (CENP-E protein).
                                            66;
                                                                                                    KINESIN-MOTOR.
COILED COIL (POTENTIAL).
GLOBULAR (POTENTIAL).
ATP (BY SIMILARITY).
MW; CEFC13880C8C8CBB CRC6
                                                                                                      MW;
                                                       Score
Pred.
                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lak I., Cleveland D.W.;
motor that accumulates
                                                        No. 0.0
                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Yen T.J., Wire
                                                                                                                                                                                                                                                                                                                                              There are no restrictions ng as its content is in
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                                                                                                                                                                                                                                                                                                                                     Usage
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                                                                                                      CRC64;
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                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CENP-E
                                                                                                                                                                                                                                                                                                                                        and
                                                                                                                                                                          Mitosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOVEMENT
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Best Local S
Matches 76
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Hypothetical 222.8 kDa protein C1F3.06C in chaspacters.06C.
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Q10411;
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
   1506
                                                                                                                                                                                                                                         1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Connor R., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.; Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-972;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces
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EAKEKIQ---VDESTIQELDHEITASKNNYEGKLNDKDSIIRDLSENIEQLNNLLAEEKS 1562
                                                           EVEEMIRDMGVGQSAVEQLAVYCVSLKKEYEN----
                                                                                                                HMLDDTSRKNSSLMEKIESINSSLDDKSFELASAVEKLGALQKLHSESLSLMENIKSQLQ 1505
                                                                                                                                                                                                                                      EDNQLATNKLKNQLDHLNQEIRLKEDVLKEKESLIISLEESLSNQRQKESSLLDAKNELE
                                                                                                                                                                                                                                                                                              EENVLDREFLKNELDNVRAQLSQKDKEKRDSQVIIDTLRDTLEERNATVVSLQQALGKAE
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                                                                                                                                                                           -MLCSTLKKQMKYLEQQQDETKQAQEEAGRLRSKMKTM------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       270690; CAA94624.1; -.
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                                                                                                                                                                                                                                                                                                                                                      Similarity 21.976; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 protein.
1957 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         366
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                                                                                                                                                                                                                                                                                                                                                            68;
                                                                                                                                                                                                                                                                                                                                                   Pred. No. 0.058; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  Score 183.5; D
Pred. No. 0.05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1957;
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RESULT 4
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01-OCT-1996
01-OCT-1996
15-JUL-1998
                                                                                                                                                                                                            Mitosis;
                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell
                                                                                                                                                              DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: ASSOCIATES WITH XCAP-E PROBABLY AS HETERODIMER.
-!- SUBCELLULAR LOCATION: NUCLEAR. DURING CHROMOSOME ASSEMBLY IN
MITOTIC EXTRACTS, XCAP-C/E WAS RECRUITED TO THE CHROMATIN AND
FORMED A DISCRETE INTERNAL STRUCTURE WITHIN ASSEMBLED CHROMOSOMES
-!- DOMAIN: CONSISTS OF TWO PUTATIVE CENTRAL COILED-COIL REGIONS
FLANKED BY PUTATIVE GLOBULAR REGIONS AT THE N- AND C-TERMINUS.
-!- SIMILARITY: BELONGS TO THE SMC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-95042742; PubMed-7954811;
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                            Pfam;
                                                                                                                                                                                                                                                                                                                                                                        EMBL; U13673; AAA64679.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       condensation in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A heterodimeric coiled-coil protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hirano T., Mitchison T.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amphibia; Batrachia;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: REQUIRED FOR BOTH ASSEMBLY AND MITOTIC CHROMOSOMES.
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                                                                                                                                                                                                                               ATP-binding;
                                                                                                                                                                                                                                                                                                IPR003439; ABC_transportr IPR003405; SMC_C. IPR003395; SMC_N.
                                                107
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841
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(Rel. 34, Last sequence up
(Rel. 36, Last annotation
                                                                                                                                                                                                                                                         SMC_N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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ATP (POTE:
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W; 2931249924FE90F6 CRC64;
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                                                                                                                                                                                                                               Nuclear protein.
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Matches 1
                                                        J. BIOI. Chem. 273:5385-5388(1998).

-: FUNCTION: GENERAL VESICULAR TRANSPORT FACTOR REQUIRED FOR INTERCISTERNAL TRANSPORT IN THE GOLGI STACK; IT IS REQUIRED FOR TRANSCYPOTIC EUSION AND/OR SUBSEQUENT BINDING OF THE VESTCLES TO THE TARGET MEMBRANE. MAY WELL ACT AS A VESICULAR ANCHOR BY INTERACTING WITH THE TARGET MEMBRANE AND HOLDING THE VESICULAR AND TARGET MEMBRANES IN PROXIMITY (BY SIMILARITY).

-: SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE PROTEIN WHICH RECYCLES BETWEEN THE CYTOSOL AND THE GOLGI APPARATUS DURING INTERPHASE.

-: DOMAIN: COMPOSED OF A GLOBULAR HEAD, AN ELONGATED TAIL (COILED-COIL) AND A HIGHLY ACIDIC C-TERMINAL DOMAIN.

-: PTM: PHOSPHORYLATED IN A CELL CYCLE-SPECIFIC MANNER; PHOSPHORYLATED IN INTERPHASE BUT NOT IN MITOTIC CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VDP_HUMAN
060763;
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND PHOSPHORY MEDLINE-98148093; Pubmed-9478999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
General vesicular transport factor pl15 (Transcytosis
                                                                                                                                                                                                                                                                      association with the Golgi membrane.";
                                                                                                                                                                                                                                                                                                       Sohda
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                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                        "Phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1023
                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                               protein) (TAP) (Vesicle
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              DEPHOSPHORYLATED PROTEIN ASSOCIATES WITH THE PHOSPHORYLATION PROMOSTES DISSOCIATION. SIMILARITY: BELONGS TO THE VDP/USO1/YBL047C F
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phorylation of the vesicle docking protein pll5 regulates
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                                                                                                                                                                                                                                                                                                                                    AND PHOSPHORYLATION SITE
             TO THE VDP/USO1/YBL047C
                                                                                                                                                                                                                                                                                                                                                                                                                                              docking
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                                                                                                                                                                                                                                                                                                                                      SER-942
                                              GOLGI MEMBRANE
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 603344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phosphorylation.
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931
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                                                  RTAIKEQLDSSNSTIAILQTEKDKLELEITDSKKEQDDLLVLLADQDQKILSLKNKLKDL
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                                                                                                                                                                                 SQLPEVEEMIRDMGVGQSA---
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                                                                                                    LQTEKQELLQKTEAFAKSVEVQGETETIIATKTTDVEGRLSALLQETKELKNEIKALSEE
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-PVEEE
                                                                                                                                                                                                                                                                                                                                                                  Conservative
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937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARM_REPEAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                 637
930
962
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942
107906
                                                                                                                                                                                                                                                                                                                                                                               7.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Armadillo
                                                                                                                                                                                                                                                                                                                                                                     62;
                                                                                                                                                                                                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                                                                                                                                                                                                                  Score 178; DB 1;
Pred. No. 0.042;
2; Mismatches 92
                                                                                                                                                                                                                                                                                                                                                                                                                                           COILED COIL (POTENTIAL).
ASP/GLU-RICH (ACIDIC).
PHOSPHORYLATION.
S->A: LOSS OF PHOSPHORYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLOBULAR HEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                   2E748F2C1BC2B942 CRC64;
                                                                                                                                                                                 -VEQLAVYCVSLK---
                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                     92;
                                                                                                                                                                                                                                                                                                                                                                                          Length 962;
                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                   142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coil;
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                        810
                                                                                                                                                                                                            750
                                                                                                                                                                                                                                    174
                                                                                                                                                                                                                                                              690
                                                                                                                                                                                                                                                                                      138
                                                                                                                                                                                                                                                                                                                                           91
                                                                            274
                                                                                                                              221
                                                                                                                                                                                 205
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MYSN_ACACA
ID MYSN_A
AC P05659
DT 01-NOV
DT 16-OCT
DE Myosin
OS Acanth
OC Eukary
OX NCBI_T
RN [1]
RP SEQUEN
RX MEDLIN
RA Hammer
RT nonmus
RT hinge
                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                      01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Myosin II heavy chain, non muscle.
Acanthamoeba castellanii (Amoeba)
                MEDLINE-87308395; PubMed-3040773;
Hammer J.A. III, Bowers B., Paterson B.M., Korn E.D.;
"Complete nucleotide sequence and deduced polypeptide sequence nonmuscle myosin heavy chain gene from Acanthamoeba: evidence c
                                                                                     SEQUENCE FROM N.A.
                                                                                                                      Eukaryota; Acanthamoebidae;
NCBI_TaxID=5755;
                                                                                                                                                                                                                                                                MYSN_ACACA
     the rodlike
                                                                                                                                                                                                                                                                 STANDARD;
   avy chain
e tail.";
                                                                                                                                                                                                            Last sequence update)
                                                                                                                                         Acanthamoeba
                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00063; myosin_head; 1. pfam; PF02736; Myosin_N; 1. pRINTS; PR00193; MYOSINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use
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                                                                                                                                                                                                                                                                                                                                          DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myosin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00612; IQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR004009; myosin_N.
InterPro; IPR001609; myosin_head
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Y00624; CAA68663.1; -. PIR; A27224; A27224.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between
                                                                                                                                                                                                                                                                                                                            DOMAIN
                             954
    148
                                                      102
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MISCELLANEOUS: THE HINGE REGION MAY PLAY A KEY ROLE IN
THE EFFECT OF HEAVY CHAIN PHOSPHORYLATION ON ENZYMATIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETI
CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF
CHARACTERISTIC OF ALPHA-HELICAL STRUCTURES. THIS F
INTERRUPTED BY A HINGE AND JOINED BY A NONHELICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell Biol. 105:913-925(1987).

FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO F-ACTIN & HAS ATPASE ACTIVITY THAT IS ACTIVATED BY F-ACTIN.

SUBUNIT: MYOSIN II HEAVY CHAIN IS TWO-HEADED. IT SELF-ASSEMBLES INTO FILAMENTS. HEXAMER OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MHC), 2 ALKALI CHAIN SUBUNITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN SIMILARITY: CONTAINS 2 IQ DOMAINS.
                                                                              DKLEKDLAALKLKILDLEGEKADLEEDNALLQKKVAGLEEELQEETSASNDILEQKRKLE
                                                                                                         NKLFFDLAQEEENVLDREFLKNELDNVRAQLSQKD------
    ETKQAQEEAGR---
                            AEKGELKASLEEEERNRKALQEAKTKVESERNELQDKYEDEAAAHDSLKKKEEDLSRELR 1013
                                                      VIIDTLRDTLEERNATVVSLQQALGKAE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P08799; 1MND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SM00015; IQ; 1
SM00242; MYSC;
                                                                                                                                      97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 non-profit institutions as long as its content is in no way d and this statement is not removed. Usage by and for commercial s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coiled
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660
766
133
700
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1494
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848
848
1227
1253
1253
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                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     Alkylation;
                                                                                                                                                                                                                                                                                                                                                                                                                    coil; Actin-binding; ATP-binding; Calmodulin-binding; lkylation; Phosphorylation; Multigene family.

MYOSIN HEAD-LIKE.
                                                                                                                                                                                                      Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                IQ;
                                                                                                                                                                                                                                819
1509
1226
1252
1509
1482
1509
189
682
780
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1489
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  ·LRSKMKTMEQIELLLQSQLPEV-EEMIRDMGVGQSAVEQLAVYCV 202
                                                                                                                                              7.48;
                                                                                                                                                                                                     171201
                                                                                                                                                                                                     MW;
                                                                                                                                                                                                                                                      ACTIN-BINDING.
ACTIN-BINDING.
METHYLATION (TRI-) (
ALKYLATION (SH-1) (F
                                                                                                                                              Score 176; DB 1;
Pred. No. 0.088;
                                                                                                                                                                                                     PHOSPHORYLATION.
W; 2CE49BE51173D17E CRC64;
                                                                                                                                                                                                                              PHOSPHORYLATION. PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                         ALPHA-HELICAL
                                                                                                                                                                                                                                                                                                                                                     LIGHT MEROMYOSIN (LMM)
                                                                                                                                                                                                                                                                                                                                                                                ALPHA-HELICAL
                                                                                                                                                                                                                                                                                                                           NONHELICAL
                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                            TAILPIECE.
                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                      TAILPIECE
                                                                                                                                     156;
                                                     ----MLCSTLKKQMKYLEQQQD 147
                                                                                                                                                                                                                                                         (POTENTIAL).
                                                                                                                                                           Length 1509;
                                                                                                                                                                                                                                                                     (POTENTIAL).
                                                                                                          -----KEKRDSQ 101
                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                              (S2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGION IS
                                                                                                                                                                                                                                                                                                                                       (LMM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HEPTAPEPTIDES,
                                                                                                                                   88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIATING
                                                                                                                                  Gaps
                                                                               953
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qγ
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       B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MYSS_CYPCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MYSS_CYPCA
Q90339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1014
                                                                                                                                                                                                  different primary structures in carp fast skeletal muscle.";
Biochem. Biophys. Res. Commun. 208:118-125(1995).
-i- FUNCTION: MUSCLE CONTRACTION.
-i- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS
-HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MHC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hirayama Y., Watabe S.; "Structural differences in the crossbridge head of temperature-associated myosin subfragment-1 isoforms from carp fast skeleta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Fast muscle
MEDLINE=97352533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, fast skeletal muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1246 -TGGASSEEVKRLEGE--LERLEEELLTA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1074
                                                                                                                                                                                                                                                                                           Watabe S., Imai J., Nakaya M., Hirayama Y., Okamoto Y., Masaki H., Uozumi T., Hirono I., Aoki T.; "Temperature acclimation induces light meromyosin isoforms with
                                                                                                                                                                                                                                                                                                                                                                                                                                           Imai J., Hirayama Y., Kikuchi K., Kakinuma M., Watabe S.;
"cDNA cloning of myosin heavy chain isoforms from carp fast skeletal
muscle and their gene expression associated with temperature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Fast muscle;
MEDLINE=97176447; PubMed=9023993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Actinopterygii; Neopterygii; Teleostei; Cypriniformes; Cyprinidae; Cyprinus.
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1387-1528 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                          acclimation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=7962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cyprinus carpio (Common carp)
                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95194396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            muscle."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301
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                                                                                                                                                                                                                                                                                                                                                                                                       Exp.
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDE: CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
PTM. TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
MISCELLANBOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QLEEE---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----VNLKLRRPSFRDDIDLNATFDVDTPPARPSSSQHGYYEKLCLEKSHSPIQDVPKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       981-1935 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -KSGKEAASSKAKQLGQQLEDARSEVDSLKSKLSAAEKSLKTAKDQNRDLDE
                                                                                                                                                                                                                                                                                                                                                                                                           200:27-34(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246:380-387(1997).
                                                                                                                                                                                                                                                                                                                                                    PubMed=7887920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=9208928;
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                                                                                                                                HEPTAPEPTIDES,
                                                                                                                                                                                                      (MLC)
                                                                                                                                                                                                                           OF.
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SIMILARITY: CONTAINS SIMILARITY: CONTAINS

1 MYOSIN-LIKE GLOBULAR HEAD 1 IQ DOMAIN.

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MOD_RES
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Pfam; PF00063; myosin_head; 1.
Pfam; PF02736; Myosin_k; 1.
Pfam; PF01576; Myosin_tail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                            1254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000048; IQ.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                           1201
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                    179
                      289
                                                                                                                                                                   136
                                                                                                                                                                                                                 79
                                                                                                                                                                                                                                                              31 LQCLIQSFETAPSRTCPQCRIQVGKRTIINKLFFDLAQEEENVLDREF------
                                                                                                                                                                                                                                                                                                     Local
DLMIDVERANSLAANLDKKQRNF
                     DRLV-LESPAPVEVNLKLRRPSF
                                             RTKYETDAIQRTEELEEAKKKL--AQR-LQDAEESIEAVNSKCASLEKTKQ--RLQGEVE 1427
                                                                   RSKLQT----VYSELDQAKLELKSAQKDLQSADKEIMSLKKKLTMLQETLNLPPVASETV
                                                                                           IEELKRHIEEEVKAKNALAHAVQSARHDCDLLREQYEEEQEAKAELQRGMSKANSEVAQW
                                                                                                                                          EDQLSEIKTKSDENVRQLNDMNAQRARLQTENGEFSRQLEEKEALV-SQLTRGKQAYTQQ
                                                                                                                                                                  KKQMKYLEQQQDETKQAQEEAGRLRSKMKT-----
                                                                                                                                                                                         VAELGEQIDNLQRVKQKLEKEKSEYKMEIDDLTSNME-----AVAKAKANLEKMCRTL
                                                                                                                                                                                                                ---LKNELDNVRAQLSQKDKEKRDSQVIIDTLRDTLEERNATVVSLQQALGKAEMLCSTL
                                                                                                                                                                                                                                         LEEISERLEEAGGATAAQIEMNKKREAEFQKMRRDL---EESTLQHEATAAALRKEQADS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D89992;
D50476;
D43700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                  -----EVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKDLFSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P08799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM00015; IQ; 1.
SM00242; MYSc;
                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS50096; IQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    family.
                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                              782
812
840
178
659
761
129
709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Methylation; Alkylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BAA22069.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1MMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BAA07802.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BAA09069.1;
                                                                                                                                                                                                                                                                                                                                                   ۶Ą,
                                                                                                                                                                                                                                                                                                                                                              781
811
839
1935
185
681
775
129
699
                                                                                                                                                                                                                                                                                                    7.3%;
22.3%;
                                                                                                                                                                                                                                                                                                                                                    221599
                                                                                                                                                                                                                                                                                         66;
                                                                                                                                                                                                                                                                                                                                                                                 HINGE.

COILED COIL (POTENTIAL).

ATP (POTENTIAL).

ACTIN-BINDING.

METHYLATION (TRI-) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                   Œ;
                      310
                                                                                                                                                                                                                                                                                                    Score 173.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                ALKYLATION (SH-1).
ALKYLATION (SH-2).
NW; 9A1244B67D63C83B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MYOSIN HEAD-LIKE
                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Calmodulin-binding;
                                                                                                                                                                                                                                                                                                   .16;
                                                                                                                                                                -MEQIELLLQSQLP-----
                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                         126;
                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                             Length 1935;
                                                                                                                                                                                                                                                                                                                                                   CRC64;
                                                                                                                                                                                                                                                                                         59;
                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                        1253
                                                                                                                                                                                                                                         1200
                                                                     288
                                                                                           1372
                                                                                                                                           1312
                                                                                                                                                                   178
                                                                                                                                                                                                                135
                                                                                                                                                                                                                                                                 78
                                                                                                                                                                                                                                                                                        11;
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RESULT RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00612; IQ; 2.
Pfam; PF00063; myosin_head; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
PF0D0m; PD000355; myosin_head; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- FUNCTION: MUSCLÉ CONTRACTION.
-!- SUBUNIT: MUSCLE CONTRACTION.
2 -!- SUBUNIT: MUSCLE (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
-!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
-!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
-!- CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
-!- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATTER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MYH4_RABIT
Q28641;
16-OCT-2001
16-OCT-2001
                                          MOD_RES
MOD_RES
MOD_RES
MOD_RES
                                                                                                                                                                       NP_BIND
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
PROSITE; PS50096; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  skeletal muscle and a novel cosynthesis of S-1 fragment essential and regulatory light chains."; Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MUSCLE CONTRACTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-NEW ZEALAND WHITE; TISSUE-Skeletal muscle; Maeda K., Hostinova E., Roesch-Kleinkauf A., Schu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Myosin heavy chain, skeletal muscle, juveni
                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                               Multigene
                                                                                                                                                                                                                                                                                                                                                       Calmodulin-binding; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                  Myosin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR004009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Isolation, sequencing of myosin heavy chain cDNA from rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wittinghofer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBFRAGMENT (S2).
SIMILARITY: CONTAINS 1
SIMILARITY: CONTAINS 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EW European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U32574; AAA74199.1;
P08799; 1MMD.
                                                                                                                                                                                                                                                                                                                                                                                  Muscle protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  non-profit
                                                                                                                                                                                                                                                                                                                                  family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                             783
813
1938
1938
186
680
774
35
130
552
756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Myosin_N.
; Myosin_tail.
; myosin_head.
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IQ.

COILED COIL (POTENT...

ATP (POTENTIAL).

ACTIN-BINDING (BY SIMILARITY).

ACTIN-BINDING (BY SIMILARITY).

ACTIN-BINDING (BY SIMILARITY).

METHYLATION (MONO-) (BY SIMILARITY).

METHYLATION (TRI-) (BY SIMILARITY).

METHYLATION (TRI-) (BY SIMILARITY).

""UVLATION (TRI-) (BY SIMILARITY).

""UVLATION (TRI-) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                  Coiled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MYOSIN-LIKE GLOBULAR HEAD DOMAIN. IQ DOMAIN.
                                                                                                                                                                                                                                                                                                       MYOSIN HEAD-LIKE
                                                                                                                                                                                                                                                                                                                                                                                  coil; Thick filament; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                       Methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       n update)
juvenile.
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                                                                                                                                                                                                                                                                                                                                                       Alkylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a collaboration -
MBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the
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RESULT HYSSULT HYSSULT
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Best Local S
Matches 86
Wagle G., Noegel A., Scheel J., Gerisch "PhosphoryLation of threonine residues Dictyostelium myosin heavy chain."; FEBS Lett. 227:71-75(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MYS2_DICDI
P08799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOD_RES
SEQUENCE
                                                                                                                                                   "Replacement of threonine residues phosphorylatable heavy chain fragme FEBS Lett. 269:239-243(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U1-NOV-1988 (Rel. 09, Created)
01-OCT-1989 (Rel. 12, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Myosin II heavy chain, non muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _DICDI
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                                                                                                                                                                                                                                                                                                                                                                            "Conserved protein domains in a myosin Dictyostelium discoideum.";
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                                                                                                                                                                                                                                  Gerisch
                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=87092266; PubMed=354
Warrick H.M., de Lozanne A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dictyostelium discoideum
                                                                                                                                                                                                                                                                           MEDLINE-90353583;
                                                                                                                                                                                                                                                      Lueck-Vielmeter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VAELGEQIDNLQRVKQKLEKEKSELKMEIDDLASNME-----TVSKAKGNLEKMCRTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQWRTKYETDAIQRTEELEEAKKKL--AQR-LQDAEEHVEAVNAKCASLEKTKQ--RLQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FSSRSKLQT----VYSELDQAKLELKSAQKDLQSADKEIMSLKKKLTMLQETLNLPPVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EDQVSELKTKEEEHQRLINDLSAQRARLQTESGEFSRQLDEKDSLVSQLSRGKQAFTQQI
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of Mg.2'(3')-O-(N-methylanthraniloy1) nucleotides bound Dictyostelium discoideum myosin motor domain.";
J. MO1. Biol. 274:394-407(1997).
-!- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO ACTIN & ACTIVITY THAT IS ACTIVATED BY ACTIN.
-!- SUBUNIT: MYOSIN II HEAVY CHAIN IS TWO-HEADED. IT SEI INTO FILAMENTS. HEXAMER OF 2 HEAVY CHAIN SUBUNITS (N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95345067; PubMed=7619796; Smith C.A., Rayment I.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gulick A.M., Bauer C.B., Thoden J.B., Raymen "X-ray structures of the MyADP, MyATPgammaS, of the Dictyostellum discoideum myosin motor Biochemistry 36:11619-11628(1997).
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MEDLINE-97452580; PubMed-9305951;
Gulick A.M., Bauer C.B., Thoden J.B.,
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Smith C.A., Rayment I.;
"X-ray structure of the magnesium(II).ADP.vanadate complex of the
"X-ray structure of the magnesium motor domain to 1.9-A resolution."
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Smith C.A., Rayment I.;
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"X-ray structure of Dictyostelium discoideum myosin to
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MEDLINE=95345066; PubMed=7619795;
Fisher A.J., Smith C.A., Thoden J.B.,
                                                          entities requires or send an email t
                                                                                                       use by non-profit institutions as modified and this statement is not re
                                                                                                                                      This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "x-ray crystal structure and solution fluorescence characterization of M9.2'(3')-O-(N-methylanthraniloyl) nucleotides bound to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dictyostelium discoideum myosin
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SIMILARITY:
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SUBCELLULAR LOCATION: HIGHEST CONCENTRATION IN
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A26655; A26655.
A26655; A26655.
S00250; S00250.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complexed with MgADP. ry 34:8960-8972(1995).
                                                                      email to license@isb-sib.ch).
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                                                                                                                                                                                                                CONTAINS
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                                                                                        a license agreement
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PDB; 1MND; 17-AUG-96.
PDB; 1MND; 17-AUG-96.
PDB; 1MND; 17-AUG-96.
PDB; 1VM; 23-DEC-96.
PDB; 1VW; 28-JAN-98.
DictyDb; DD01008; mbcA.
DictyDb; DD010048; IQ.
InterPro; IPR000409; Myosin_N.
InterPro; IPR001609; myosin_head.
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Pfam; PF02736; Myosin_N; 1.
Pfam; PF02736; Myosin_N; 1.
PRINTS; PR00193; MYOSINHBAYY.
PRODom; PD000355; myosin_head; 1
SMART; SM00015; IQ; 1.
SMART; SM000242; MYSC; 1.
                                RA50_AQUAE
067124;
16-0CT-2001
16-0CT-2001
16-0CT-2001
        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable DNA double-strand break repair rad50
RAD50 OR AQ_1006.
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                                                                                                                                                                                                                                   RVRLQ---SELDDLTVRLDSETKDKSELLRQKKKLEEELKQVQEAL----AAETAAKLA
                                                                                                                                                                                                                                                           RSKLQTVYSELDQAKLELKSAQKDLQSADKEIMSLKKKLTMLQETLNLPPVASETVDRLV
                                                                                                                                                                                                                                                                                                                                 LALENLQNQKRSVE------
                                                                                                                                                               PKKICKGPRKESQLSLGGQSCAGEPDEE
                                                                                                                                                                                                                                                                                   YEEELEEMKR-VNDGQSDTISRLEKIKDELQKEVEELTES--FSEESKDKGVLEK----T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00612; IQ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                             90;
 aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         7.2%;
nilarity 27.4%;
Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    762
817
179
638
738
130
1678
1823
1823
2029
2116
                                                                                                                                                                                      -ANKKLQ---
                                                                               STANDARD;
                                                                                                                                          ESQL----VAVNNELDEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,
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791
2116
186
660
752
130
678
1823
1823
1823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243871
                                                                                                                                                                                        -GEYTELNEKFNSEV-TARSN---
                                                                                                                                                                                                                                                                                                                                                                                                                          49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METHYLATION (DI-) (
ALKYLATION (SH-1).
PHOSPHORYLATION (BY
PHOSPHORYLATION (BY
PHOSPHORYLATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IQ.
COILED COIL (PATP.
ACTIN-BINDING.
ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 172;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYOSIN HEAD-LIKE.
                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                        ore 172; DB 1; Length 2116; ed. No. 0.2; Mismatches 109; Indels 8
                                                                                                                                                                                                                                                                                                                                -EKVRDLEEELQEE-----QKLRNTLEKLKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPHORYLATION (BY MHCK).
SPHORYLATION (BY MHCK).
SPHORYLATION (BY MHCK).
2FC3770BB1EE56Al CRC64;
                                                                                                                                          1106
                                                                                                                                                                380
                                                                               978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                       ATPase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
                                                                                                                                                                                      -VEKSKKTL---
                                                                                                                                                                                                                                                                                                                                                                                                                          80;
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                                                                                                                                                                                      1092
                                                                                                                                                                                                                                     1056
                                                                                                                                                                                                                                                                                   1004
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                                                                                                                                                                                                                                                                                                                                                                             911
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TANA\_XENLA Q01550; Q1-JUN-1994 Q1-JUN-1994 16-OCT-2001

(Rel. (Rel. (Rel.

29, Created)
29, Last sequence update)
40, Last annotation updat

STANDARD;

PRT;

1744

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RESULT 11
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR003439; ABC_transportr.

DNA repair; Hydrolase; ATP-binding; Coiled coil; Components of the control of the coil o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for concentities requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aqu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE000718; AAC07092.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 392:353-358(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aeolicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Aquificales; Aquificaceae; Aquifex.
NCBI_TaxID=63363;
                                                                                                                         746 EIEEKLK-----EYEGIRELSDIKGEYESVKTQLEEKHKKLGEVKREL
                                                                                                                                                                                     309
                                                                                                                                                                                                                                                689
                                                                                                                                                                                                                                                                                                                                                                       639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              541 MEKLRNEVEELRKE-----IPENLKER---IKKLEELRIEKEKLEHKLNKYRKAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 APSRTCPQCRIQVGKRTIIN-----KLFFDLAQEEENVLDREF-----LKNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
SUBUNIT: Forms a complex with mrell (By similarity).
SIMILARITY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Involved in DNA double-strand break repair (DSBR). The rad50/mrell complex possesses single-strand endonuclease activity and ATP-dependent double-strand-specific exonuclease activity. Rad50 provides an ATP-dependent control of mrell by unwinding
                                                                                                                                                                                 SFRDDIDLNATFDVDTPPARPSSSQHGYYE--KLCLEKSHSPIQDVPKKI
                                                                                                                                                                                                                                                                                                                                                                                                               VSLKKEYENLKEARKASGEVADKLRK---DLFSSRSKLQTVYSELDQAKLELKSAQKDLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQQQDETKQAQEEAGRLRSKMKTMEQIELLLQSQL-PEVEEMIRDMGVGQSAVEQLAVYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboratic sen the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                SLEEERKEKLKELANIYEVAKSP----REVVELYLGDKEAELERKIKEFEESFQSLKLKKS
                                                                                                                                                                                                                                                                                                        SADKEIMSLKKKLTMLQETLNLPPVASETVDRLVLESPAPVE-----VNLKLRRP
                                                                                                                                                                                                                                                                                                                                                                       ESLKEEINYINSKLQEIEEKEKKLRKHFEELSSRKSKLEG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDROKOKEEAQAKLHKAQTELELLKE-KIREKSRLVKEFKELYR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDNVRAQLSQKDKEKRDSQVIIDTLRDTLEERNATVVSLQQALGKAEMLCSTLKKQMKYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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22.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76;
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RESULT
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Matches 61
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MYH3_RAT
P12847;
01-OCT-1989
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SEQUENCE
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and formaticities are not to be a supported by and formaticities are not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Amphibia; Batrachia; Anura; Mo
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M99387; AAA49966.1; PIR; JH0720; JH0720.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <del>-</del>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities
                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001664; IF.
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                                                                                                               141
                                                                                                                                  179
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                                                                                                                                                       81
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                                                                                                                                                                                                                    67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tities requires a license agreement (Seend an email to license@isb-sib.ch).
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                                                                                                                                                                                                                AQEEENVLDREFLKNELDNVRAQLSQKDKEKRDSQVIIDTLRDTLEERNATVVSLQQALG
                                                                      EEYKSEVSVLEAGLSESKENLRKVLEENKQNRLLLQSLDKELVSLKMRKEALEDLLS
                                                                                                              ELEDILRDHEEEKALMEE---EIASFSQRLENFRVAPVAFKPVEVDDYARKLSEIWQGAV
                                                                                                                                 EVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKA--SGEVADKLRK--DLFSS--
                                                                                                                                                       QAEMVRDSIYEEIEFVKQRCLEEKQAREDAKKELSESKKLLEEETRAQIWLKERLGQLEA
                                                                                                                                                                        KAEMLCSTLKKQMKYLEQQQDETKQAQEEAGRLRSKMKTMEQIELLLQSQL-----P
                                                                                                                                                                                               ALEEEN----ELLRKEIHSLRSSKSERCWKKKHHEEMM-KLRDALDDGHREMV-----
                                                                                                                                                                                                                                                                                                                                                                                                                          PF00038;
                                                                                                                                                                                                                                        61;
                                                                                         -RSKLQTVYSELDQAKLELKSAQKD-----
                                                                                                                                                                                                                                                 Similarity
(Rel. 12, Created)
                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                             49
61
157
180
194
                                                                                                                                                                                                                                                                                                                                                                                              filament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              head;
                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                            filament;
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1744
48
60
156
179
179
193
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                                                                                                                                                                                                                                                  25
                                                                                                                                                                                                                                                 7.1%;
25.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                     Coiled
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                                                                                                                                                                                                                                                                                                                    COIL 1A.
LINKER 1.
COIL 1B.
LINKER 12.
COIL 2A.
                                                                                                                                                                                                                                              Score 169.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                 LINKER
COIL 2B
                                                                                                                                                                                                                                                                                                                                                                                                    coil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
                     PRT;
                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                        6502EAC9FE6C4E93 CRC64;
                                                                                                                                                                                                                                                                                                  28
                                                                                                                                                                                                                                                                                                             2
                                                                                                                                                                                                                                                                                                                                                                                                     Neurone
                    1940 AA
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                                                                                        --LOSADKEIMSLKKKLTMLQETLN
                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                      74;
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                                                                                                                                                                                                                                                          1744;
                                                                                                                                                                                                                                      39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            outstation
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                                                                     254
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                                                                                                                                 232
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-:- FUNCTION: MUSCLE CONTRACTION:
-:- SUBUNIT: MUSCLE CONTRACTION:
-:- SUBUNIT: MUSCLE CONTRACTION:
-:- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
-:- REQUARMORY LIGHT CHAIN SUBUNITS (MLC-2)
--- AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2)
--- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
--- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
--- CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
--- CYCLES OF A 28-RESIDUE REPLICAL COLLED COILS.
--- CYCLES OF A 28-RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY
--- ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
--- MISCELLANEOUS: EACH MYOSIN HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
SPLIT FUNT 1 LIGHT
MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
SPLIT FUNT 1 CONTROL OF THE STATEMENT CONTROL OF THE STATEME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         myosin
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MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1989
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                 Pfam; PF02736; Myosin_N; 1. Pfam; PF01576; Myosin_tail;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A24922; A2492;
HSSP; P08799; 1MND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=87060988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myosin heavy
                                                                                                                                                                                                      Calmodulin-binding;
                                                                                                                                                                                                                                                                                              ProDom; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                     PRINTS; PR00193;
                                                                                                                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00612; IQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute.
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                                                                      DOMAIN
                                                                                                                                DOMAIN
                                                                                                                                                  DOMAIN
                                                                                                                                                                     DOMAIN
                                                                                                                                                                                     Multigene
                                                                                                                                                                                                                          Myosin;
                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                SMART;
                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002017; InterPro; IPR001609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete nucleotide and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nadal-Ginard B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the rod."
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SIMILARITY: CONTAINS 1 MYOSIN-LIK
SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                            PF00063; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X04267; CAA27817.1;
                                                                                                                                                                                                                                                         SM00015; IQ; 1.
SM00242; MYSc;
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                                                                                                                                                                                                                        Muscle protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR002928;
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Strehler-Page M.-A.,
AA;
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; Myosin_N.
; Myosin_tail.
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                                                                                                                                                                                                      ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Spectrin.
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                                                                                                                                                                                                                          Coiled coil;
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               METHYLATION (TRI-) (POTENTIAL). ALKYLATION (SH-1). ALKYLATION (SH-2).
                                                                      ACTIN-BINDING ACTIN-BINDING
                                                                                                           COILED COIL (POTENTIAL) ATP (POTENTIAL).
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B5D546A596E5A696 CRC64;
                                                                                                                                                                                                    bil; Thick filament; Actin-binding;
Methylation; Alkylation;
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                                                                               SEQUENCE OF 1871-1935 FROM N
STRAIN-WISTAR; TISSUE-Heart;
MEDLINE-85179510; PubMed-624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MYH7_RAT P02564;
and under pathological conditions
availability.";
                                      MEDLINE=85179510; PubMed=6241892;
Mahdavi V., Lompre A.M., Chambers A.P., Nadal-Ginard B.;
"Cardiac myosin heavy chain isozymic transitions during
                                                                                                                                                                                                                                                                                                                            McNally E.M., Kraft R., Bravo-Zehnder M., "Full-length rat alpha and beta cardiac my Comparisons suggest a molecular basis for J. Mol. Biol. 210:665-671(1989).
                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90133919; PubMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90016823; PubMed=2798112;
Kraft R., Bravo-Zehnder M., Taylor D.,
"Complete nucleotide sequence of full ]
cardiac myosin heavy chain.";
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1139
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                                                                                                                                                                                                                  Mahdavi V., Periasamy M., Nadal-Ginard "Molecular characterization of two myos
                                                                                                                                                                                                                                                             MEDLINE-82220036;
                                                                                                                                                                                                                                                                                   SEQUENCE OF 1524-1935 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Heart;
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MYH7.
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01-OCT-1989 (Rel. 12,
16-OCT-2001 (Rel. 40,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus
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                                                                                                                                                                                                                                                             PubMed-7045682;
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Rodentia;
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ardiac muscle beta isc
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Pred. No. 0.
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chain sequences
differences.";
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                                                                                                                                                                                                               genes
                    level
                                        development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65;
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                    0f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
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Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000048;
InterPro; IPR004009;
InterPro; IPR002928;
InterPro; IPR001609;
                                                          MOD_RES
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                   MOD_RES
MOD_RES
MOD_RES
                                                                                                                                                                                  NP_BIND
                                                                                                                                                                                                                                                                                                                  Pfam; PF00063; myosin_head; 1. Pfam; PF02736; Myosin_N; 1. Pfam; PF01576; Myosin_tail; 1. PRINTS; PR00193; MYOSINHBAYY. PT000m; PD000355; myosin_head; PT000m; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removentitles requires a license agreement (Sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for
                                                                                                                                                                                                                                                                                                         SMART;
                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                              Galmodulin-binding.
                                                                                                                                                                                                                                                           ATP-binding;
                                                                                                                                                                                                                                                                       Myosin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                               SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP;
           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (MIC), 2 ALKALI LIGHT CHAIN SUBUNITS (MIC), AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MIC-2).

SUBCELLULAR LOCATION: Thick filaments of the myofibrils. SUBCELLULAR RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISCELLANEOUS: THE CARDIAC ALPHA ISOFORM IS A 'FAST' ATFASE MYOSIN, WHILE THE BETA ISOFORM IS A 'SLOW' ATFASE. SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN. SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
MISCELLANGOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . Heart J. 5:181-191(1984). FUNCTION: MUSCLE CONTRACTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPLIT FURTHER INTO SUBFRAGMENT (S2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       S06006; S06006.
A02989; A02989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X15939; CAA34065.1;
J00752; AAA41654.1;
M32698; AAA41659.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                              P08799;
                                                                                                                                                                                                                                                                                              SM00015; IQ; 1.
SM00242; MYSC;
65; Conser
                                                                                                                                                                                                                                                                       Muscle
                                                                                                                                                                                                                                                                                   PS50096; IQ;
                                                             1529
1731
1784
1851
1858
1935
                                                                                                                                   781
840
178
655
757
729
695
705
                                                                                                                                                                                                                                                         Methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                              1MMD
                                                                                                                                                                                                                                                                       protein;
                                                             Ã
                                                            780
810
1935
.
185
677
771
129
695
705
705
1531
1731
1731
1734
1858
1858
           7.18;
22.58;
                                                                                                                                                                                                                                                                                                                                                                                           myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                        Myosin_tail.
                                                                                                                                                                                                                                                                                                                                                                                                                   Myosin_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GLOBULAR SUBFRAGMENTS
                                                                                                                                                                                                                                                                       Coiled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . . . .
                                                                                                                                                                                                                                                           Alkylation;
                                                             MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agreement (See
        Score
Pred.
                                                                       METHYLATION ()
ALKYLATION ()
IRK -> VRR ()
IRK -> VRR (IN R)
D -> H (IN R)
N -> K (IN R)
T -> N (IN R)
                                                                                                                                                                       ATP.
ACTIN-BINDING.
ACTIN-BINDING.
                                                                                                                                                                                                           IQ.
COILED
                                                                                                                                                                                                                                  MYOSIN HEAD-LIKE
                                                                                                                                                                                                                                                                       coil;
                                                            > N (IN REF. 3).
> K (IN REF. 3).
C8376C324A7BD82B
           169;
No. 0.
                                                                                                                                                                                                           COIL
                                                                                                                                                                                                                                                                       Thick filament;
                                                                                                                                                                                                                                                         Multigene
                                                                       ON (TRI-) (POTENTIAL).

(N (SH-1) (POTENTIAL).

(N (SH-2) (POTENTIAL).

(R (IN REF. 3).

N REF. 3).

N REF. 3).

N REF. 3).

N REF. 3).
            . 26;
                      DB
                                                                                                                                                                                                            (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . Usage by and fo http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (S1) AND 1 ROD-SHAPED
                        Length 1935;
                                                                                                                                                                                                                                                          nent; Actin-binding;
family;
                                                             CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch/announce/
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31 LQCLIQSFETAPSRTCPQCRIQVGKRTIINKLFFDLAQEEENVLDREF----

Matches

Conservative

62;

Mismatches

106;

Indels

56;

Gaps

9;

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Q9Z1Z0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOUSE
                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
General vesicular transport factor pl15 (Transcytosis associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1143
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                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein) (TAP) (Vesicle
 Phosphorylation.
                      Transport; Protein
                               PROSITE; PS50176; ARM_REPEAT;
                                                      InterPro; IPR000225; Armadillo.
InterPro; IPR000219; RhoGEF.
                                                                            MGD; MGI:1929095; Vdp.
                                                                                        EMBL;
                                                                                                             or send
                                                                                                                          entities
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233
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                                                                                                                                                                                                                                                                                                                                                                                                             S.J.
                                                                                                                                                                                                               DOMAIN: COMPOSED OF A GLOBULAR HEAD, AN ELONGATED TAIL (COIL COIL) AND A HIGHLY ACLOIC C-TERMINAL DOMAIN.
PTM: PHOSPHORYLATED IN A CELL FORCIFIC MANNER;
PHOSPHORYLATED IN INTERCHASE BUT NOT IN MITOTIC CELLS.
DEPHOSPHORYLATED PROTEIN ASSOCIATES WITH THE GOLGI MEMBRANE;
PHOSPHORYLATION PROMOSTES DISSOCIATION (BY SIMILARITY).
                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE VDP/USO1/YBL047C FAMILY.
                                                                                                                                                                                                                                                                                   SIMILARITY)
                                                                                                                                                                                                                                                                                               BETWEEN THE CYTOSOL AND THE GOLGI APPARATUS DURING
                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboratic een the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no we by non-profit institutions as long as its content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKQMKYLEQQQDETKQAQEEAGRLRSKMKT------MEQIELLLQSQLP-------
: || : :| | :: | |:|::| :: | |: || ||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VAELGEQIDNLQRVKQKLEKEKSEFKLELDDVTSNMEQ-----IIKAKANLEKMCRTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---LKNELDNVRAQLSQKDKEKRDSQVIIDTLRDTLEERNATVVSLQQALGKAEMLCSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RTKYETDAIQRTEELEEAKKKL--AQR-LQDAEEAVEAVNAKCSSLEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RSKLQT----VYSELDQAKLELKSAQKDLQSADKEIMSLKKKLTMLQET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEDLKRQLEEEVKAKNALAHALQSARHDCDLLREQYEEETEAKAELQRVLSKANSEVAQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----EVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKDLFSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDQMNEHRSKAEETQRSVNDLTRQRAKLQTENGELSRQLDEKEALI-SQLTRGKLTYTQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEEISERLEEAGGATSVQIEMNKKREAEFQKMRRDL---EEATLQHEATAAALRKKHADS
                                                                                        AF096868; AAC72967.1; -.
                                            SM00325; RhoGEF;
                                                                                                              an email to license@isb-sib.ch).
                                                                                                                        requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s (Mouse).
Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                      transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               docking protein) (Fragment).
                     UNKNOWN_1.
Golgi stack;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; E
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  941
                      Membrane;
                                                                                                                                     Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murinae;
                      Coiled
                                                                                                                                                                                                                                                                                                                                                                                               protein/p115).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              277
                                                                                                                                                                                                                                                                                               INTERPHASE
                                                                                                                                     and
                                                                                                                                                                                a collaboration
                                                                                                                                                                                                                                                                         (COILED
                                                                                                                                     for
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RESULT
G160_MC
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DOMAIN
DOMAIN
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                    Golgin-160 (Male-enhanced antigen-2) (MEA-2). GOLGA3 OR MEA2.
                                                                                                                                                                                                                                                                   STRAIN=CD-1; TISS
MEDLINE=97217683;
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
15-DEC-1998 (Rel. 37, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOUSE
                                                                                                                                                autoantigen.";
DNA Seq. 7:71-82(1997).
-i- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN
TESTIS DEVELOPMENT. PROBABLY IDENTICAL W
                                                                                                                                                                                                                "Cloning and molecular characterization of cDNA encoding male-enhanced antigen-2 (Mea-2): a putative family of the
                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G160_MOUSE
                                                                                                                                                                                                                                                       Kondo M., Sutou S.
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                               DETECTABLE MALE ANTIGEN (SDM).
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS.
FOUND IN SPERMATIDS DURING SPERMATOGENESIS. NO
LEYDIG CELLS, SPERMATOGONIA, OR SPERMATOCYTES.
SIMILARITY: HIGH, TO HUMAN GOLGIN-160.
CAUTION: IT IS UNCERTAIN WHETHER MET-1, MET-19
 SWISS-PROT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALSEERTAIQKQLDSSNSTIAILQTEKDKLDLEVTDSKKEQDDLLVLLADQDQKILSLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QALLQGQLAEKDSLIENLKSSQASGMSEQASATCPPRDPEQVAELKQELTALKSQLCSQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVTQQASQIQQHKDQYNLLKVQLGKDNHHQGSHGDGAQVNGIQPEEISRLREEIEELKSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --TKQAQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSEEDKKEEEV----KKTLEQHDNIVTHYKNMIREQDLQLEELKQQVSTLKCQNEQLQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QKDKEKRDSQVIIDTLRDTLEERNATVVSLQQALGKAEMLCSTLKKQMKYLEQQQDE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIGKENFIEKLGFISKHELYSRASQKPQPNFPSPEYMIFDHEFTKLVKELEGVITKAIYK 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLKDLGH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLTMLQETLNLPPVASE 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASGEVADKLRKDLFSSRSKLQTVYSELDQAKLELKSAQKD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEITRLQTENCELLQRAETLAKSVPVEGESEHVSAAKTTDVEGRLSALLQETKELKNEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELLLQSQLPEVEEMIRDMGVGQSA--VEQLAVYC----
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7683; PubMed=9063644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -PVEEE
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912 CO
941 ASI
922 PH
105152 MW;
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19.6%;
18
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copyright.
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PHOSPHORYLATION (BY SIMILARITY).
R; AB5C10895CD7E508 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 168; DB Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLOBULAR HEAD.
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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WITH THE SEROLOGI
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                                                                                                    EXPRESSION
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RESULT 16
MYH2_HUMAN
ID MYH2_H
AC Q9UKX2
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DT 16-OCT
DT 16-OCT
DT 16-OCT
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GN MYH2 O
OS HOMO
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OC MAMMAI
OX MEDLIN
RP SEQUEN
RX MEDLIN
RA Weiss
RT heavy
RL J. MO1
RN [2]
RP SEQUEN
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RY SEQUEN
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Best Local S
Matches 77
                                                                                                                                                                                                                                                 Q9UKX2; Q16229; Q14322;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Myosin heavy chain, skeletal muscle, adult
                                                                                    SEQUENCE FROM N.A.
TISSUE=Skeletal muscle;
MEDLINE=99318869; PubMed=10388558;
Meiss A., Schiaffino S., Leinwand
                                                                                                                                                                                                                                                                                                                                                                                                                         1306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@ish-aih
                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1193
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the Euro
                 SEQUENCE
                                                            Weiss A., Schiaffino S., Leinwand L.A.; "Comparative sequence analysis of the complete human sarcomeric myosin heavy chain family: implications for functional diversity.";
                                                                                                                                                                                                                                   MYH2 OR MYHSA2
                                                                                                                                                                                                                                                                                                                                           MYH2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1136
   TISSUE=Skeletal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD;
                                                                                                                                                                                                                    Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   PKKICKGPRKESQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSKEPLK-NLNNCLQQLKQEMDSLQRQMEEHTITVHESLSSWAQVEAAPAEHAH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----PVEVNLKLRRPSFRDDID-LNATFDVDTPPARPSSSQHGYYEKLCLEKSHSPIQDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NMKTLLQQNQQLKLDLRRGAAKKKEPKGESNSSSPATPIKIPDCPVPASLLEELLRPPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KL-TMLQET----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLKQQLDLTEQQG----KKELEGTQQTLQTIKSELEMVQEDLSETQKDKFMLQAKVSELKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NLKEARKASGEVADKLRKDLFSSRSKLQTVYSELDQAKLELKSAQKDLQSADKEIMSLKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KQAQEEAGRIRSKMKTMEQIELLIQSQLPEVEEMIRDMGVGQSAVEQLAVYCVSIKKEYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEQMAAARIEAGHNRRHFKAATLELSEVKKELQAKEHLVQTLQAEVDELQIQDGKHSQEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQALGKA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REHNSILETALAKREADLYQLNLQVQAVLQRKEEEDRQMKQLVQALQVSLEKEKMEVNSL
                                              chain family: implications l. Biol. 290:61-75(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P18852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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1325 AA;
                   1711-1941 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                        PRGDTKL 1312
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                                                                                                                                                                                                                                                                                                                           STANDARD;
; Q14322;
                                                                                                                                                                                      Chordata;
Primates;
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149880 MW;
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Pred. No. 0.19;
55; Mismatches 1
                                                                                                                                                                                      Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3230636962C687B0 CRC64;
                                                                                                                                                                                                                                                                                                                                            1941
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adult 2
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                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                      Hominidae;
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                                                                                                                                                                                                   Euteleostomi;
                                                                                                                                                                                        Homo
                                                                                                                                                                                                                                                              heavy
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31 LQCLIQSFETAPSRTCPQCRIQVGKRTIINKLFFDLAQEEENVLDREF---

58;

Score 168; DB Pred. No. 0.29 58; Mismatches

DB 1;

Length 1941;

106;

Indels

62;

Gaps

9

Query Match Best Local S Matches 66

ch 7.0%; l Similarity 22.6%; 66; Conservative 9

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STITITION OF THE STANDERS OF T
NP_BIND
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000048;
InterPro; IPR004009;
InterPro; IPR002928;
InterPro; IPR001609;
InterPro; IPR001609;
Pfam; PF00612; IQ; 2.
                                                                                                                                                                                                                      SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
PROSITE; PS50096; IQ; 1.
                                                                                                                                                                          Calmodulin-binding; ATP-binding; Methylation;
                                                                                                                                                                                                      Myosin; Muscle protein;
                                                                                                                                                                                                                                                                                                                                                                                Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collal between the Swiss Institute of Bioinformatics and the EMBL outs the European Bioinformatics Institute. There are no restrictions
                                                                             DOMAIN
                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                              ProDom; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                        PRINTS; PR00193;
                                                                                                                                                                                                                                                                                                                                                    Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM; 160740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <del>-</del> --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  myosin heavy chains they express.";
J. Muscle Res. Cell Motil. 16:35-43(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Skeletal muscle;
MEDLINE=95270723; PubMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Type IIx myosin heavy chain transcripts fibers of human skeletal muscle."; Am. J. Physiol. 267:C1723-C1728(1994).
                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ennion S., Sant'ana Pereira J., Sarque Characterization of human skeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smerdu V., Karsch-Mizrachi I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1823-1941 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schiaffino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBERAGMENT (S2).
SIMILARITY: CONTAINS 1 MYOSIN-LIKE SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF : HEAVY CHAIN SUBUNITS (MIC), 2 ALKALI LIGHT CHAIN SUBUNITS (MIC), AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MIC-2).

SUBCELLULAR LOCATION: Thick filaments of the myofibrils. SUBUNIS SUBCELLULAR LOCATION: TRICK FILAMENTS OF THE MYOFIBRILS. SHOWING DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PYM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATANSE ACTIVITY.

MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: MUSCLE CONTRACTION
                                                                                                                                                                                                                                                                                                                     PF02736; Myosin_N; 1.
PF01576; Myosin_tail; 1.
S; PR00193; MYOSINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF111784; AAD29950.1; -. S73840; AAC13916.1; -.
                                                                                                                                                                                                                                                                                                                                                                      PF02736; Myosin_N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P08799; 1MND.
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MEDLINE-93165084; PubMed=7679477;
Dahmen A., Gallin M., Schumacher M., Erttmann
Dahmen A., Gallin M., Schumacher M., Erttmann
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Mol. Biochem. Parasitol. 57:335-338(1993).
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FUNCTION: PARAMYOSIN IS A MAJOR STRUCTURAL COMPONENT OF MANY THICK FILAMENTS ISOLATED FROM INVERTEBRATE MUSCLES SUBUNIT: HOMODIMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Thick filaments of the myofibrils
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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in; Thick filament; Myosin.
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CONHELICAL REGION (POTENTIAL).
NONHELICAL REGION (POTENTIAL).
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IS A MAJOR STRUCTURAL COMPONENT
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"Identification of paramyosin as a potential protective antigen
against Brugia malayi infection in jirds.";
MO1. Biochem. Parasitol. 49:315-324(1991).

-i- FUNCTION: PARAMYOSIN IS A MAJOR STRUCTURAL COMPONENT OF
MANY THICK FILAMENTS ISOLATED FROM INVERTEBRATE MUSCLES.

-i- SUBGNIT: HOMODIMER (BY SIMILARITY).
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01-FEB-1996 (Rel. 33, Created)
15-JUL-1998 (Rel. 36, Last seguence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                between the Swiss Institute of Bloinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 180-263 AND 684-880 FROM N.A. MEDLINE=92131068; PubMed=1775173;
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Submitted
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NCBI_TaxID=6279;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -- EMLCSTLKKQMKYLEQQQ----DETKQAQEEAGRLRSKMKTM---
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                                      U77590;
м63097;
                                                                                              s requires a license agreement (S an email to license@isb-sib.ch).
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                  AAC18613.1;
AAA27859.1;
AAA27860.1;
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Best Local
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                                                       MYSA_DROME
P05661;
01-NOV-1988
01-JUN-1994
16-OCT-2001
Eukaryota; Me
Pterygota; Ne
Ephydroidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                    -----DSQVIIDTLRDTLEERNATVVSLQQALGKA-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF01576;
                                                                                                                                                                                                                                                                                                                                            -EQIELLLQSQLPEVEEMIRDMGVGQ------
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                                               neavy
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                           melanogaster (Fruit fly).
           Neoptera;
                   Metazoa; Arthropoda;
                                                      (Rel. 09,
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(Rel. 40,
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          Endopterygota;
                                                                                                                                         TDLVSVN----NNLTAIKN--KLETELSTAQADLD
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19
                                                      Last sequence update)
Last annotation updat
                                                                        Created)
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NONHELICAL REGION (POTENTIAL).

V -> I (IN REF. 2).

D -> A (IN REF. 2).

L -> F (IN REF. 2).

E -> Q (IN REF. 2).

A -> R (IN REF. 2).

A -> R (IN REF. 2).

HOLLRAKMLQROKFTFSKMSNRDN -> SS'

IYVLEDEQ (IN REF. 2).

HYVLEDEQ (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 167; DB Pred. No. 0.13; 89; Mismatches
  Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NONHELICAL REGION
                                                                                            PRT;
                   Tracheata; Hexapoda; Insecta;
                                                                                                                                                                            ----KVALDNAIRARKQAEIDLEEAN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   filament;
          Diptera;
                                                                                            2411
                                                       update)
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                                                                                                                                                                                                                                                   ----EIDRLTAALADAEARMK
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          Brachycera;
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          Muscomorpha;
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                                                                                                                                                           464
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EMBL;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=89384556; PubMed=2506434;
George E.L., Ober M.B., Emerson C.P. Jr.;
George E.L., Ober M.B., Emerson C.P. Jr.;
"Functional domains of the Drosophila melanogaster muscle myosin "Functional domains of the Drosophila melanogaster muscle myosin heavy-chain gene are encoded by alternatively spliced exons.";
heavy-chain gene are encoded by alternatively spliced exons.";
"~~11. Biol. 9:2957-2974(1989).
                                                       This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for conmodified and this statement is not removed.
                                                                                                                                                                                                                                                       EMBO J. 10:2479-2488(1991).

IN SUBUNIT: MUSCLE CONTRACTION.

IN SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

IN SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

IN SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN SUBUNITS (MLC)

AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

IN SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

IN ALTERNATIVE PRODUCTS: AS DROSOPHILA HAS A SINGLE MUSCLE MHC GENE, MHC ISOFORMS MUST RELY ON ALTERNATIVE RNA SPLICING THAT LEADS TO DIFFERENCES IN THE C-TERMINUS OF THE VARIOUS MHC PROTEINS.

IN MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S2).

SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.

SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-312 FROM N.A.
MEDLINE-87280141; PubMed-3038896;
Wassenberg D.R. II, Kronert W.A., O'Donnell P.T., Bernstein S.
"Analysis of the 5' end of the Drosophila muscle myosin heavy
gene. Alternatively spliced transcripts initiate at a single s
intron locations are conserved compared to myosin genes of oth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    splicing mutation in an alternative
substitution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       intron locations
organisms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kronert W.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CANTON-S; TISSUE=Embryonic MEDLINE=91330870; PubMed=1907912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Muscle-specific accumulation of Drosophila myosin heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 486-881 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chem. 262:10741-10747(1987).
                                  requires
email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Edwards K.A., Roche E.S.,
                                                                                                                                                                                                                                         (S2).
CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
CONTAINS 1 IQ DOMAIN.
                                  a license agreement
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                               (See http://www.isb-sib
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FlyBase; FBgn0002741; N InterPro; IPR000048; IC InterPro; IPR000409; My InterPro; IPR002928; My InterPro; IPR001609; My PRINTS; PR00193; ProDom; PD000355; SMART; SM00015; I0 SMART; SM00242; M BL; M61229; AAA286861.1; ABL; M61229; AAA28607.1; ABL; M61229; AAA28706.1; ABL; J02788; AAA28707.1; ABL; X60196; CAA427753.1; ABL; X60196; CAA42753.1; ABL; X60196; CAA42754.1; ABL; X60196; CAA42754.1; ABL; X60196; AAA291. n; PF00612; IQ; 2.
n; PF00663; myosin\_head; 7.
n; PF00736; Myosin\_N; 1.
n; PF01576; Myosin\_tail; 1.
nr; PF01576; Myosin\_tail; 1. P08799; PD000355; myosin\_head; 1MND IQ. myosin\_head Myosin\_N. Myosin\_tail ALT\_SEQ
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PAM_STRY 20
PAM_STRY ID PAM_S
AC P4905
AC P4905
DT 01-FE
DT 01-FE
DT 16-OC
DE PLASH
GN PAM.
OS Streg
OC Streg
RN [1]
RP SEQUIT
RN [2]
RP SEQUIT
RX MEDL.
RX MEDL.
RX MEDL.
RX BEGGG
RT "PAM
RT DYOG
RL J. B
CC -1-
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Best Local S
Matches 93
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P49054;
01-FEB-1996
01-FEB-1996
16-OCT-2001
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VARSPLIC
CONFLICT
              pyogenes.
J. Biol.
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                             Berge A., Sjoebring U.; "PAM, a novel plasminogen-binding protein progenes.":
                                                             SEQUENCE FROM N.A., AND SEQUENCE STRAIN-AP53 / Serotype M53; MEDLINE-94064605; PubMed-8244975;
                                                                                                                                                   Streptococcus pyogenes
                                                                                                                                                                            Plasminogen-binding
                                                                                                                                                                                                                                                                                                        2377
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Myosin; Muscle pro
                                                                                                                                       Bacteria; Firmicutes;
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                                                                                                              NCBI_TaxID=1314;
                                                                                                                             Streptococcus
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  FUNCTION: BINDS
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              Chem.
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                                                                                                                                                                                      (Rel. 33, Created)
(Rel. 33, Last sequence update)
(Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96; IQ; 1.
protein; (
              268:25417-25424(1993)
                                                                                                                                                                                                                                         STANDARD;
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234
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TO HUMAN PLASMINOGEN. COULD PROVIDE THE BACTERIA
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                                                                                                                                      Bacillus/Clostridium group; Streptococcaceae;
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                                                                                      SEQUENCE
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COILED COIL (POTENTIAL).
ATP (BY SIMILARITY).
P -> I (IN SHORT ISOFORM).
MISSING (IN SHORT ISOFORM).
EK -> RE (IN REF. 2).
EK -> RE (IN REF. 2).
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Pred. No. 0
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                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                            precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                         388
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                                    from
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                                     Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2411;
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Best Local
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PROSITE;
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                                                                                                                                                                                                                                                                                                                                   NON_TER
SEQUENCE
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                           REPEAT
REPEAT
DOMAIN
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DOMAIN
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InterPro; IPR003345; M_repeat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
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381
                 368
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SUBCELLULAR LOCATION: CELL WALL ASSOCIATED SIMILARITY: TO OTHER STREPTOCOCCAL AND STAI IN THE REGION OF THE MEMBRANE ANCHOR.
г
                    r
                                                                                                                                                                                                                   TLRDTLEERNATVVSLQQALGKAEMLCSTLKKQMKYLEQQQDETKQAQEEAGRLRSKMKT
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                                                                                          AEELAKLRAEKASDSQTPDAKPGN---
                                                         A-----TFDVDTPPARPSSSQHGYYEKLCLEKSHSPIQDVPKKICKGPRKESQLS
                                                                                                                                       RKDLFSSRSK-----LQTVYSELDQAKLE-----
                                                                                                                                                           EKQISDASRQGLR-----
                                                                                                                                                                              MEQIELLLQSQLPEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKL
                                                                                                                                                                                                   KLADKQEHLNGA-----QKKLKE
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                                                                              EEANSKLAALEKLNKELEES-
                                                                                                                     RRDLDASREAKKQVEKGLANLTAELDKVKEEKQISDASRQGLRRDLDASREAKKQVEKAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF02370; M; 8.
TE; PS00343; GRAM_POS_ANCHORING;
                  368
                                                                                                                                                                                                                                                                                 l Similarity
73; Conserv
 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Repeat;
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388
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20
91
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104
147
                                                                                                                                                                                                                                                                                 Conservative
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116
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1161
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161
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380
386
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43629
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                                                                                                                                                           RDLDASREAKKQVEKDLANLTAELDKVKEEKQISDASRQGL
                                                                                                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                                                                                                                                62;
                                                                                                                                                                                                                                                                                                                                                              C-2.
C-3 (INCOMPLE
GLY/PRO-RICH.
CONSERVED IN
                                                                                                                                                                                                                                                                                           Score 166; DB 1
Pred. No. 0.059;
                                                                                                                                                                                                                                                                                                                                                                                                      B-2.
3 X TANDEM REPEATS,
C-1.
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8-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OR 28 (POTENTIAL).

PLASMINOGEN-BINDING PROTEIN PAM
2 X APPROXIMATE TANDEM REPEATS,
                                                                                                                                                                                                                                                                                                                                                       PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                               ×
                                                                                                                                                                                                                                                                                                                                   EEEC4FD962CCDB12 CRC64
                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              TANDEM REPEATS,
                                                                                                                                                                                                                                                                                                                                                                                   (INCOMPLETE).
                                                                             --KKLTEKEKAELQAKLEAEAKALKEQLAKQ
                                     ·KAVPGKGQAPQAGTKPNQNKAPMKETKRQ
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                                                                                                                                                                                                                                                                                                                                                                Z
                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                GRAM-POSITIVE COCCI SURFACE
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                                                                                                                                                                                                                                                                                  120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Usage
                                                                                                                                                                                                                                                                                                    Length 388;
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE
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CONFLICT
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SEQUENCE
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DOMAIN
                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VDP_RAT STANDARD; PRT; , 959 AA.
P41542;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
General vesicular transport factor p115 (Transcytosis associated protein) (TAP) (Vesicle docking protein).
                                                                                                                                                                           InterPro; IPR000225; Armadillo
PROSITE; PS50176; ARM_REPEAT;
                                                                                                                                                                                                           EMBL; U14192; AAA62632.1; -. EMBL; U15589; AAC52151.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               factor required for binding of vesicles to acceptor membranes.";

Proc. Natl. Acad. Sci. U.S.A. 92:527-531(1995).

-I. FUNCTION: GENERAL VESICULAR TRANSPORT FACTOR REQUIRED FOR INTERCISTERNAL TRANSPORT IN THE GOLGI STACK; IT IS REQUIRED FOR TRANSCYTOTIC FUSION AND/OR SUBSEQUENT BINDING OF THE VESICLES TO THE TARGET MEMBRANE. MAY WELL ACT AS A VESICULAR ANCHOR BY INTERACTING WITH THE TARGET MEMBRANE AND HOLDING THE VESICULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-95132633; PubMed=7831324; Parroso M.. Nelson D.S., Sztul E.;
                                                                                MOD_RES
                                                                                                                               DOMAIN
                                                                                                                                               Phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-95132632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Transcytosis-associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "pll5 is a general vesicular transport factor
                                                                                                                                                                                                                                                                                                                                                                                                                   COILED-COIL TAIL. DIMER FORMED BY PARALLEL ASSOCIATION OF THE TAILS.

SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE PROTEIN WHICH RECYCL BETWEEN THE CYTOSOL AND THE GOLGI APPARATUS DURING INTERPHASE. BOMAIN: COMPOSED OF A GLOBULAR HEAD, AN ELONGATED TAIL (COILED COIL) AND A HIGHLY ACIDIC C-TERMINAL DOMAIN.

PTM: PHOSPHORYLATED IN A CELL CYCLE-SPECIFIC MANNER; PHOSPHORYLATED IN INTERPHASE BUT NOT IN MITOTIC CELLS. DEPHOSPHORYLATED PROTEIN ASSOCIATES WITH THE GOLGI MEMBRANE; DEPHOSPHORYLATED PROTEIN ASSOCIATES WITH THE GOLGI MEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21
                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION PROMOSTES DISSOCIATION (BY SIMILARITY). SIMILARITY: BELONGS TO THE VDP/USO1/YBL047C FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND TARGET MEMBRANES IN PROXIMITY.
SUBUNIT: HOMODIMER WITH TWO N-TERMINAL HEADS AND A C-TERMINAL COILED-COIL TAIL. DIMER FORMED BY PARALLEL ASSOCIATION OF THE
                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through
en the Swiss Institute of Bioinformatics and the El
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lasmic reticulum to Golgi transport factor Usolp. Natl. Acad. Sci. U.S.A. 92:522-526(1995).
                                                                                                                                                                                              IPR000225; Armadillo.
                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=7831323;
Walter D.M., Grosvenor A.R.,
                  637
930
959
940
591
658
816
                                                                                                                                                              transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
 107162
 ₩,
                          COILED COIL (POTENTIAL).
ASP/GLU-RICH (ACIDIC).
PHOSPHORYLATION (BY SIMILARITY).
S -> P (IN REF. 2).
M -> V (IN REF. 2).
S -> R (IN REF. 2).
                                                                                                                              GLOBULAR HEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                            Golgi stack; Membrane;
                                                                                                                                                                               UNKNOWN_1
356394B48C7E003B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TAP)/pl15 is a general fusion
                  s x
                Q I N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  crelated to
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 CRC64;
                                                                                                                                                            Coiled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J.E
                                                                                                                                                                                                                                                                                                                                         EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                          a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (COILED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RECYCLES
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RESULT ;

WYH7_PIG
ID WYH7
PT 15---
DT 15--
DT 15---
DT 1
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                                                                                                                                                                                                      Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.

C: -: FUNCTION: MUSCLE CONTRACTION.

C: -: SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

C: -: SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

C: HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)

C: AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

C: -: SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

C: OMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

C: -: PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY ALKILATED AND ARE REQUIRED FOR MYOSIN APPASE ACTIVITY.

C: MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED CRUMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  p79293;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Cardiac muscle beta isoform (MyHC-beta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ko Y.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-DOMESTICA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         270 KLTMLQETLNLPPVASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22
                                                        MISCELLANEOUS: THE CARDIAC ALPHA ISOFORM IS A 'FAST' ATH MYOSIN, WHILE THE BETA ISOFORM IS A 'SLOW' ATPASE. SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                SUBFRAGMENT (S2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASGEVADKLRKDLFSSRSKLQTVYSELDQAKLELKSAQKD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELLLQSQLPEVEEMIRDM-----GVGQSAV-----EQLAVY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSEEDKKEEEV----KRTLEQHDNIVTHYKNMIREQDLQLEELKQQVSTLKCQNEQLQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIGKENYIEKLGFISKHELYSRASQKPQPNFPSPEYMIFDHEFTKLVKELEGVITKAIYK 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLKDLGH----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEITRLQTENSELQQRAETLAKSVPVEGESELVTAAKTTDVEGRLSALLQETKELKNEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVLLQSQLAEKDTVIENLRSSQVSGMSEQALATCSPRDAEQVAELKQELSALKSQLCSQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVTQQASQIQQHKDQYNLLKVQLGKDNHHQGSHSDGAQVNGIQPEEISRLREEIEELRSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --TKQAQ------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Suina; Suidae; Sus.
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20.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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There are no restrictions

and the EMBL

outstation

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Pfam; PF00063; myosin_had; 1.
Pfam; PF02736; myosin_lv; 1.
Pfam; PF01576; myosin_tail; 1.
PRINTS; PR00193; mYOSINHEAVY.
PRODOM; PD000355; myosin_head; 1
SMART; SM00015; IQ; 1.
SMART; SM00015; MYSC; 1.
i_HUMAN

MYH1_HUMAN

P12882; 099622;

01-OCT-1989 (Rel. 1
16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                       NP_BIND
DOMAIN
DOMAIN
MOD_RES
MOD_RES
MOD_RES
                                                                                                                                                1514
                                                                                                                                                                                          1457
                                                                                                                                                                                                                                      1403
                                                                                                                                                                                                                                                                                 1347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; Myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch)
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                                                                                                    1551
                                                                                                                                                                                                                                                                                                                            1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Calmodulin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P08799;
                                                                                                                                                                                                                237
                                                                                                                                                                                                                                                            187
                                                                                                                        349
                                                                                                                                                                                                                                                                                                                                                  79
                                                                                                                                                                                                                                                                                YEEETETKAELQRVLSKANSEVAQWRTKYETDAIQRTEELEEAKKKLAQRLQDAEE----
                                                                                                                                                                                                                                                                                                   LKKQMKYLEQQQDETKQAQEEAGRLRSKMKT------MEQIELLLQSQLPEVEEMIRD 186
                                                                                                                                                                                                                                                                                                                           LSRQLDEKEALISQLTRGKLTYTQQLEDLKRQLEEEVKAKNALAHALQSARHAADLLREQ 1346
                                                                                                                                                                                                                                                                                                                                                LKNELDNVRAQLSQKDKEKRDSQVIIDTLRDTLEE----RNATVVSLQQALGKAEMLCST 134
                                                                                                  LEHEEGKILRAQLEFNQIKAEMERKLAEKDEEM
                                                                                                                                                                  DRLVLESPAPVEVNLKLRRPSFRDDIDLNATFDVDTPPARPSSSQHGYYEKLCLEKSHSP 348
                                                                                                                                                                                                               QTVYSELDQAKLELKSAQKDLQSADKEIMSLKKKL---
                                                                                                                                                                                                                                                          MGVGQSAVEQLAVYCVSLKK-----EYENLK----EARKASGEVADKLRKDLFSSRSKL
                                                                                                                       IQDVPKKICKGPRKESQLSLGGQSCAGEPDEEL
                                                                                                                                             EQLGSSGKTIHELE-KVRKQLEAEKLELQS---
                                                                                                                                                                                          KQKYEE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U75316; AAB37320.1;
                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS50096; IQ;
                                                                                                                                                                                                                                     -AVEAVNAKCSSLEKTKHRLQNETEDLMVDVERSNAAAAALDKKQRNFDKILAEW
                                                                                                                                                                                                                                                                                                                                                                                                                            781
839
178
655
757
729
129
695
705
                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Methylation;
                                                                                                                                                                                          -SQSELESSQKEARSLSTELFKLKNAYEESLEHLETSKRENKNLQEEISDLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein; Coiled
                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                              Ã,
 12,
40,
                                                                                                                                                                                                                                                                                                                                                                                                                                        780
810
1935
185
677
771
129
695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 license agreement (See http://www.isb-sib.ch/announce/
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Last sequence up
                      Created)
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                                                                                                                                                                                                                                                                                                                                                                       62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IQ.
COILED COIL (POTENTIAL).
ATP (POTENTIAL).
ACTIN-BINDING.
ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                              WW
                                                                                                                                                                                                                                                                                                                                                                      Score 166; DB
Pred. No. 0.37
52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      METHYLATION (TRI-) (POTENTIAL) ALKYLATION (SH-1) (POTENTIAL). ALKYLATION (SH-2) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MYOSIN HEAD-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coil;
                                                                                                                                                                                                                                                                                                                                                                                                                            149CDBFD910DBB08
                                             1939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thick filament; Actin-binding; 
; Multigene family;
                                                                                                  1583
                                                                                                                       381
                                            ΑA
                                                                                                                                                                                                                                                                                                                                                                                DB
.37;
                                                                                                                                                                                                                                                                                                                                                                      131;
                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                -TMLQETLNLPPVASETV
                                                                                                                                                                                                                                                                                                                                                                                          Length 1935;
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NUCLEIC ACIDS RES. 14:2951-2969(1986).

11 FUNCTION: MUSCLE CONTRACTION.

11 SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

12 SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

13 SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)

AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

14 SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

15 SUBCELLULAR RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COLLED COLLS.
         DOMAIN
NP_BIND
DOMAIN
DOMAIN
MOD_RES
MOD_RES
                                                                                                                                                                                                             SMART;
                                                                                                                                                                                                                        Pfam; PF00063; myosin_head; 1.
Pfam; PF01576; Myosin_tail; 2.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weiss A., Schiaffino S., Leinwand L.A.;
"Comparative sequence analysis of the complete human sarcomeric myosin heavy chain family: implications for functional diversity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Skeletal muscle;
MEDLINE=99318869; PubMed=10388558;
Weiss A., Schiaffino S., Leinwand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Myosin
IIx/d)
                                                                                                                                                                                                                                                                                      InterPro; IPR000048; IQ.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saez L., Leinwand L.A.;
"Characterization of diverse forms of myosin heavy chain expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                 Myosin; Muscle protein;
                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                   PIR; A23767; A23767.
HSSP; P03437; 1HTM.
                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF111785; AAD29951.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adult human skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=86176778;
                                                                                                         DOMAIN
                                                                                                                      DOMAIN
                                                                                                                                                Calmodulin-binding; ATP-binding; Methylation;
                                                                                                                                                                                                                                                                                                                                        MIM; 160730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S2).
SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                heavy chain, skeletal muscle, adult 1 (Myosin heavy chain (MyHC-IIx/d).
                                                                                                                                                                                              SM00015; IQ; 1.
SM00242; MYSC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OF 1064-1939 FROM
                                                                                                                                                                                   PS50096; IQ;
                                                                                                                                     family
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843
179
659
761
130
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PubMed=2421254;
            784
814
1939
186
681
775
130
                                                                                                                                                                 Coiled coil;
COILED COIL (POTENTIAL)
ATP (POTENTIAL).
ACTIN-BINDING (BY SIMACTIN-BINDING (BY SIMACTHYLATION (TRI-) (INTEXTACTION (SH-1) (P. 1)
                                                                                                                      MYOSIN HEAD-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                 Thick filament; Actin-binding;
                         G (BY SIMILARITY).
G (BY SIMILARITY).
(TRI-) (POTENTIAL)
                                                                                                                                                   Alkylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
; Homo.
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Best Local s
Matches 84
(1)
SEQUENCE FROM N.A.
MEDLINE=20057165; Pubme-
Dunham I., Hunt A.R., C
Dunham I., Smink L.J., I
                                                                                                                                               MYH9_HUMAN STANDARD; rn., P35579; O60805; O1-JUN-1994 (Rel. 29, Created) 15-DEC-1998 (Rel. 37, Last sequence update) O1-MAR-2002 (Rel. 41, Last annotation update) Myosin heavy chain, nonmuscle type A (Cellular myosin Myosin heavy chain, heavy chain-A) (NMMHC-A).
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                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FSSRSKLQT-----VYSELDQAKLELKSAQKDLQSADKEIMSLKKKLTMLQETLNLPPVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKQMKYLEQQQDETK------QAQEEAGRL-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EELKR----QLEEEIKAKSALAHALQSSRHDCDLLREQYEEEQEAKAELQRAMSKANSEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELLLQSQLPEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                HGYYEKL----CLEKSHSPIQ----
                                                                                   s (Human).
Metazoa; Chordata; C
Metazoa; Primates; C
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    PubMed=10591208;
.R., Collins J.E.
.J., Ainscough R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 166; DE
Pred. No. 0.37
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALKYLATION
A -> T (IN
Q -> L (IN
G -> V (IN
A -> T (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VS -> 1
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                                                                                                Craniata; Vertebrata;
Catarrhini; Hominidae
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    Bruskiewich
Almeida J.P
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.37;
                                                                                                   Hominidae;
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۰۰
    R., Beare
., Babbage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
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RA COVILIG G.J., COX A.V., Davis J., Dawson E., Dhami P.D., Dockned C., RA Dodsworth S.J., Durbin R.M., Ellington A., Evans K.L., Fey J.M., RA Fleming K., French L., Garner A., Gilbert J.G.R., Goward M.E., RA Fleming K., French L., Garner A., Gilbert J.G.R., Goward M.E., RA Fleming K., French L., Garner A., Gilbert J.G.R., Goward M.E., RA Grafham D., Griffiths M.N., Hall C., Hall R., Hall-Tamlyn G., RA Heathcott R.W., Ho S., Holmes S., Hunt S.E., Jones M.C., Kershaw J., RA Heathcott R.W., Ho S., Holmes S., Hunt S.E., Jones M.C., Kershaw J., RA Holyd C., Lloyd D.M., Martyn I.D., Mashreghi-Mohammadi M., RA Lloyd C., Lloyd D.M., Martyn I.D., Mashreghi-Mohammadi M., Ra Milnes S.A., Mortimore B.J., Odell C.N., Pavitt R., Pearce A.V., Pavitt R., Pearce A.V., Rogers L., Kosan R. M., Pavitt R., Pearce A.V., Ra Ramsey Y., Rogers L., Kosan T., Scott C.E., Sebra H.K., Skuce C.D., Smith M.L., Soderlund C., Spragon L., Steward C.A., Smalley S., Smith M.L., Soderlund C., Spragon L., Steward C.A., Smalley S., Smith M.L., Soderlund C., Spragon L., Steward C.A., Williams S., Kosan R., Kan Ramsey Y., Rogers J., Shintani A., Shibuya K., Yoshizaki Y., Aoki T., RA Mitsuyama S., Koe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Williams S., Kan Ramseki K., Sasaki T., Ra Hai H., Lao H.I., Lewis J., Lewis S., Lin S.-P., Loh P., Hua A., Kenton S., RA Lai H., Lao H.I., Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Ra Munt P., Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Ra Bourne S., Cordes M., Du Z., Fulton L., Goela D., Graves T., Ra Hawkins J., Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Ra Bourne S., Cordes M., Du Z., Fulton L., Goela D., Graves T., Ra Budarf M.L., Kim U.J., Shizuya H., Simon M.I., Saitta S., Ra Peyrard M., Kedra D., Seroussi E., Fransson I., Tapla I., Bruder C.E., The DNA Sequence of human chromosome 22.*; Hu X., Hu X., Li L., Li L.
                                                                                                        Mhatre
"Human
                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 714-1960 FROM N.A.
MEDLINE=90138958; PubMed=1957836;
MEDLINE=90138958; PubMed=1957836;
MEDLINE=90138958; PubMed=1957836;
MEDLINE=90138958; PubMed=1957836;
MEDLINE=90138958;
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDITINE=91316803; PubMed=1860190; Simons M., Wang M., McBride O.W., Kawamoto S., Gdula D., Adelstein R.S., Weir L.; "Human nonmuscle myosin heavy chains are encode on different chromosomes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bagguley C., Bailey J., Barlow K., Bates K.N., Beasley O., Bird C. Blakey S., Bridgeman A.M., Buck D., Burgess J., Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G., Clegg S.M., Cobley V., Cole C.G., Collier R.E., Connor R.E., Conroy D., Corby Cobley V., Cole C.G., Collier R.E., Connor R.E., Conroy D., Corby C., Collier R.E., Connor R.E., Conroy D., Collier R.E., Collier R.E., Collier R.E., Conroy D., Collier R.E., Collier R.E., Collier R.E., Collier R.E.,
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Circ. Res. 69
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MEDLINE=91316803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Toothaker L.E., Gonzalez D.A., Tung N., Lemons R.S., le Beau M.M. Arnaout M.A., Clayton L.K., Tenen D.G.; "Cellular myosin heavy chain in human leukocytes: isolation of 5'cDNA clones, characterization of the protein, chromosomal
                                                                    nonmuscle myosin MYH9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               localization, and upregulation during myeloid Blood 78:1826-1833(1991).
                                                                                                                                                                                     Lalwani A.K.,
                                                                                                                                                                                                                             MEDLINE=20489856;
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                                                                                                                                             A.N.;
                                                                                                        nonsyndromic hereditary deafness
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                                Genet.
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                                                                                                                                                                                 PubMed=11023810;
Istein J.A., Kelley
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                                67:1121-1128(2000)
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differentiation.";
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TRANSPORTATION OF THE PROPERTY OF THE PROPERTY
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-I- SUBUNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LICHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

-I- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

-I- DISEASE: DEFECTS IN MYH9 ARE THE CAUSE OF MAY-HEGGLIN ANOMALY (MHA), AN AUTOSOMAL DOMINANT MACROTHROMBOCYTOPENIA CHARACTERIZED BY THROMBOCYTOPENIA, GIANT PLATELETS AND LEUKOCYTE INCLUSIONS.

-I- DISEASE: DEFECTS IN MYH9 ARE THE CAUSE OF FECHYNER SYNDROME (FTNS), AN AUTOSOMAL DOMINANT MACROTHROMBOCYTOPENIA CHARACTERIZED BY THROMBOCYTOPENIA, GIANT PLATELETS AND LEUKOCYTE INCLUSIONS.

MITH ADDITIONAL ALPORT-LIKE CLINICAL FEATURES OF SENSORINEURAL DEAFNESS, CATARACTS AND NEPHRITIS.

-I- DISEASE: DEFECTS IN MYH9 ARE THE CAUSE OF SEBASTIAN SYNDROME (SBBSOTHAD GRANT MACROTHROMBOCYTOPENIA CHARACTERIZED BY THROMBOCYTOPENIA, GIANT PLATELETS AND LEUKOCYTE INCLUSIONS.

-I- DISEASE: DEFECTS IN MYH9 ARE THE CAUSE OF SEBASTIAN SYNDROME (SBBSOTHAD GRANT MACROTHROMBOCYTOPENIA CHARACTERIZED BY THROMBOCYTOPENIA CHARACTERIZED BY THROMBOCYTOPENIA CHARACTERIZED CHARACTERIZED BY PROGRESSIVE HEARING IMPAIRMENT AND COCHLEOSACCULAR DEGENERATION.

-I- STMILBATTEV. COUNTAINS 1 MYCHNIE HEARING IMPAIRMENT AND COCHLEOSACCULAR DEGENERATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seri M., Cusano M., Gangarossa S., Caridi G., Bordo D., Lo Nigro C Ghiggeri G.M., Ravazzolo R., Savino M., Del Vecchio M., d'Apolito Iolascon A., Zelante L.L., Savia A., Balduini C.L., Noris P., Magrini U., Belletti S., Heath K.E., Babcock M., Clucksman M.J., Aliprandis E., Bizzaro N., Desnick R.J., Martignetti J.A.; "Mutations in WH9 result in the May-Hegglin anomaly, and Fechtner Sebastian syndromes".
                                                                                                                                                                                                                                                                                                                                                                                                                                MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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MEDLINE-20428193; PUBMed-10973260;
Kelley M.J. Jawien W., Ortel T.L., Kor
"Mutation of MYH9, encoding non-muscle
                                                                                                                                                                                                                                                                                                                                         MIM;
                                                                                                                                                                                                                                                                                                                                                                                                   MIM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch)
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Nat. Genet. 26:106-108(2000).
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                                                                                                                                                                                                            InterPro;
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IL; M69105; AAA59888.1; -.
IL; M69180; AAA61765.1; -.
IL; M31013; AAA36349.1; -.
IP; P08799; ILVK.
I; 160775; -.
II; Z82215; CAB05105.1; -.
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                                                                                                                                            rrPro; IPR000048; IQ.
rrPro; IPR004009; Myosin_N.
rrPro; IPR002928; Myosin_tail.
rrPro; IPR002017; Spectrin.
rrPro; IPR001609; myosin_head.
n; PF00612; IQ; 1.
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PF01576;
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PD000355;
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myosin_head; 1.
Myosin_N; 1.
Myosin_tail; 1.
93; MYOSINHEAVY.
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DOMAIN
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ion; Multigene family; Disease muta
                               /FTId=VAR_010797.

EAII -> RGH (IN REF. 3).

T -> M (IN REF. 4).

T -> M (IN REF. 4).

C -> Y (IN REF. 4).

KG -> GR (IN REF. 2).

E -> EE (IN REF. 2).

T -> A (IN REF. 2).

S -> G (IN REF. 2).

S -> G (IN REF. 2).
Score 166;
Pred. No. 0
                                                                                                                                                                                                    ALAXIDAN (SH-1) (POTENTIAL)
ALKYLATION (SH-2) (POTENTIAL)
N -> K (IN MHA).
FFTTA-VIF
                                                                                                           D -> H (IN FTNS).
/FTId=VAR_010796.
E -> K (IN MHA).
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/FTId=VAR_010793.
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R -> C (IN FTNS).
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/FTId=VAR_010795
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/FTId=VAR_010794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QCRIQVGKRTIINKLFFDLAQEEENVLDREF------LKNELDNVRAQLSQK
VDLDHQRQSACNLEKKQKKFDQLLAEEKTI 1456
                                                                                                                                                       APVEVNLKLRRPSFRDDIDLNATFDVDTPPARPSSSQHGYYEKLCLEKS----HSPIQDV
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                                                          KKKMEDSVGCLETAEEVKRKLQKDLEGLS---QRHEEKVAAYDKLEKTKTRLQQELDDLL
                             - PKRPRSESSCSKDVVRTGFDGLGGRTKFI
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                                                                                         ·CKGPRKESQLSLGGQSCAGEPDEELVGAFPIFVRNAILGQKQ-----
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BPA1_HUMAN S:
Q03001; Q13775;
01-OCT-1996 (Rel
16-OCT-2001 (Rel
Tang H.-Y., Chaffotte A.-F., Thacher S.M.;

"Structural analysis of the predicted coiled-coil rod domain or cytoplasmic bullous pemphigoid antigen (BPAGI). Empirical localization of the N-terminal globular domain rod boundary.";

J. Biol. Chem. 271:9716-9722(1996).

-!- FUNCTION: COMPONENT OF HEMIDESMOSOME PLAQUE. THE PROTEINS PROBABLY SELF-AGGREGATE TO FORM FILAMENTS OR A TWO-DIMENSIMESHWORK. POTENTIAL INTERACTION WITH KERATIN INTERMEDIATE
                                                                                                                                                                                                                                                               TISSUE-Keratinocytes;
MEDLINE-89067122; PubMed-2461961;
Stanley J.R., Tanaka T., Mueller S.,
"Isolation of complementary DNA for l
of patients' autoantibodies.";
J. Clin. Invest. 82:1864-1870(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          constituent protein as a dit epithelia.";
                                                                                                                                                                                               MEDLINE=96199235; PubMed=8621649;
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1777-2704 FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diaz L.A., Franke W.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1650-2257 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Comparison of molecularly cloned bullous desmoplakin I confirms that they define a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Keratinocytes;
MEDLINE-91286285; Pub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Elgart G.W., Stanley J.K.;
"Cloning of the 5' mRNA for the 230-kD bullous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BPAL HUMAN STANDARD; PRT; 2704 AA. Q3001; Q13775; Q9UGD8; Q9UGD7; Q1-QCT-1996 (Rel. 34, Created) 16-QCT-2001 (Rel. 40, Last sequence update) 16-QCT-2001 (Rel. 40, Last annotation update) Bullous pemphigoid antigen 1 (230 kDa bullous
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Differentiation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-91216368;
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Chem. 266:12555-12559(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parry D.A.D., Klaus-Kovtun V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dermatol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tion of a second protein product of the gene encoding rmal autoantigen.";
300:851-857(1994).
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    Characterization 
fferentiation marker

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-! SUBUNIT: HOMODIMER.
-! ALTERNATIVE PRODUCTS: 4 ISOFORMS; 1, 2, 3 (SHOWN HERE) AND BE PRODUCED BY ALTERNATIVE SPLICING.
-! DISEASE: INVOLVED IN THE SUBEPIDERWAL BLISTERING DISEASE BULLOUS PEMPHICOID, AN AUTOIMMUNE DISEASE.
-! SIMILARITY: CONTAINS 10 PLECTIN REPEATS.
-! SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-! SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-! SIMILARITY: CONTAINS 4 SPECTRIN REPEATS.
-! SIMILARITY: BELONGS 70 THE PLAKIN OR CYTOLINKER FAMILY.
-! CAUTION: ISOFORMS 2 AND 4 ARE FRAGMENTS AT THE N-TERMINUS.
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DOMAIN
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PROSTITE, PSSONOW, SH3, FALSE_NEG.
Antigen; Coiled coil; Repeat; SH3 domain; Structural protein;
Antigen; Coiled coil; Repeat; SH3 domain; Structural protein;
Cytoskeleton; Cell adhesion; Alternative splicing.
Cytoskeleton; Cell adhesion; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SMART; SM00150; SPEC; 3
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MIM; 113810;
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AL096710;
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OOATEGYAGIRCENFTTCWRDKLFNAIIKKYRDLLDMFU
VAVQSNLANLEHAFYVAEKIGVIRLLDPEDVDVSSPDEKSV
ITYVSSLYDAFPKVPEGGEGIGANDVEVKWIEYQNMVNYLI
                                                                       QWIRHHYTTMSERTFPNNPVELKALYNQYLQFKETEIPPKE
TEKSKIKRLYKLLEKVFCFLKIWIEFGRIKLLQGYHPNDIE
KEWGKLIIAMLEREKALRPEVE (IN ISOFORM 1).
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p25386;
01-MAY-1992 (Rel. 22, Cres)
01-MAY-1992 (Rel. 22, Las)
16-CCT-2001 (Rel. 40, Las)
Intracellular protein tranusol or INT1 OR YDL058W.
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CONFLICT
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                                                                  "A cytoskeleton-related gene, uso1, protein transport in Saccharomyces of Cell Biol. 113:245-260(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1433
                                                                                                           макајіma Н., Hirata
Yamasaki М.;
                                                                                                                          MEDLINE-91185402; PubMed=2010462;
Nakajima H., Hirata A., Ogawa Y.,
                                                                                                                                                         STRAIN=X2180-1A
                                                                                                                                                                                                Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                                                                                                           Eukaryota; Fungi;
                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1606
  Submitted
                 Kendrick K.E.
                             Hostetter M.K.,
                                         SEQUENCE OF 782-1790 FROM N.A.
                                                                                                                                                                      SEQUENCE FROM N.A.
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  (FEB-1993) to the
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1998
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Last annotation update)
transport protein USO1.
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                          D.J.,
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G -> R (IN REF. 5).
MW; A7219E687A634A77 CR
  EMBL/GenBank/DDBJ databases
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8; Mismatches
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Pred. No. 0
                           Bendel C.M.,
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                                                                                                                           Yonehara
                                                                                  cerevisiae.
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                                                                                                 is required
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                             McClellan
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SEQUENCE OF 1-8 FROM N
Bai Y., Symington L.S.
Submitted (MAY-1996) t
-!- FUNCTION: REQUIRED
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SGD; S0002216; USO1.
InterPro; IPR002017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X54378; CAA38253.1;
EMBL; L03188; AAB00143.1;
EMBL; U53668; AAB66659.1;
PIR; A38455; A38455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                             103
  308
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DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE OF AN HEPTAPEPTIDE REPEAT PATTERN CHARACTERISTIC OF A COILED COILS. MAY FORM FILAMENTOUS STRUCTURES IN THE SIMILARITY: BELONGS TO THE VDP/USO1/YBL047C FAMILY.
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PSFRDDIDLNATFDVDTPPARPSSSQHGYYEK----
                                           QKDLQSADKEIMSLKKKLTMLQETLNLPPVASETVDRLVLESPAPVEVN----
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                         QEKIRINAEENTVLKSKL-----
                                                                      LEQSKXSAEEDIKNLQHEKSDLISRINESEKDIEELKSKLRIEAKSGSELETVKQELNNA
                                                                                             LKEARKASGEVADKLR-------
                                                                                                                       SKAKVEEGLKKLEEESSKEKAELEKSKEMMKKL---ESTIESNETELKSSMETIRKSDEK
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                                                                                                                                             EAGRLRSKMKTMEQIELLLQSQLPEVEEMIRDMGVGQSAVE---
                                                                                                                                                                                                                                                                   78; Conservative
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ed (MAY-1996) to
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E -> K (IN REF. 2)
V -> I (IN REF. 2)
V -> I (IN REF. 2)
N -> S (IN REF. 2)
G -> S (IN REF. 2)
I -> V (IN REF. 2)
R -> S (IN REF. 2)
D -> DEEDDEE (IN REF. 2)
D -> DEEDDEE (IN REF. 2)
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                                                                                                                                                                                                                                                                              Score 165.5; D
Pred. No. 0.36;
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CHARGED (HYPER-HYDROPHILIC).
DISPENSABLE FOR THE PROTEIN
ASP/GLU-RICH (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLOBULAR HEAD
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                         ---EDIERELKDKQAEIKSNQEEKELLTSRL
                                                                                           -KDLFSSRSKLQTVY - - - SELDQAKLELKSA
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                                                                                                                                                                                                                                                                                          DB 1;
-LCLEKSHSPI --
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p13392;
01-JAN-1990 (Rel. 13, 0
01-JUN-1994 (Rel. 29, 1
01-MAR-2002 (Rel. 41, 1
                                                                                                                                                                                                                        DISULFID
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           paramyosin."
Mol. Biochem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Dirofilaria immitis (Canine heartworm).
Eukaryota, Metazoa; Nematoda; Chromador
Onchocercidae; Dirofilaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This
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MEDLINE-89344126; PubMed-2527335;
Grandea A.G. III, Tuyen L.K., Asikin N., Davis T.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIRIM_
                                                                                                                                                                                                                                                                                                     DISULFID
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Pfam; PF01576; Myosin_tail; 1.
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PIR; A44972; A44972.
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"A lambda gtll cDNA recombinant that
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-90220759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=6287;
     171
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                                                     59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. Parasitol. 35:31-41(1989).
FUNCTION: PARAMYOSIN IS A MAJOR STRUCTURAL COMPONENT MANY THICK FILAMENTS ISOLATED FROM INVERTEBRATE MUSCI SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Thick filaments of the myofibrils SIMILARITY: HIGH, TO MYOSIN HEAVY CHAINS.
INKLFFDLAQE-----EENVLDREF--LKNELDN---VRAQLSQKDKEKR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Parasitol. 38:271-280(1990).
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J04009; AAA28300.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P80220; 1DIP
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; Thick filament; Myosin.
                                                                                                Score 165; DB
Pred. No. 0.16;
0; Mismatches
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NONHELICAL REGION (POTENTIAL).
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similarity).
SUBUNIT: For
SIMILARITY:
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Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Klenk H.-P., Clayton R.J., Gwinn M., Hickey E.K., Peterson J.D., Retchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Richardson D.L., Coackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Feterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archaea; Euryarchaeota; Archaeoglobus.
                                                                                                                                                                                                                                                          Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               029230;
                                                                                                                                                        "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-98049343; PubMed-9389475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-VC-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archaeoglobus fulgidus.
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16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
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                                                                                           FUNCTION: Involved in DNA double-strand break repair (DSBR). rad50/mrell complex possesses single-strand endonuclease act
                             rad50/mrell complex possesses single-strand endonuclease activity
and ATP-dependent double-strand-specific exonuclease activity.
Rad50 provides an ATP-dependent control of mrell by unwinding
and/or repositioning DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RTGFDGLGGRTKFIQPTDTVMIRPLPVKPKTKVKQRVRVKTVPSLFQAKLD
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NGS TO THE SMC FAMILY. RAD50 SUBFAMILY

BELONGS

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Best Local
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RA50_PYRAB
Q9UZC8;
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                                        Pyrococcus abyssi.
Archaea; Euryarchaeota;
NCBI_TaxID=29292;
                                                                                                16-OCT-2001 (Rel. 40, Cr
16-OCT-2001 (Rel. 40, La
16-OCT-2001 (Rel. 40, La
DNA double-strand break
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 SEQUENCE FROM STRAIN-ORSAY;
                                                                                      RAD50 OR PAB0812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repair; Hydrolase; ATP-binding; Coiled coil; Complete BIND 31 38 ATP (BY SIMILARITY). AIN 148 728 COILED COIL (POTENTIAL). UBNCE 886 AA; 103633 MW; D35641D499AA8B58 CRC64;
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97; Conservative
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IPR002017;
               N.A
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Last annotation updat
ak repair rad50 ATPase
                                                       Thermococcales; Thermococcaceae;
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Pred. No. 0.
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ATPase.
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Best Local S
Matches 61
                                                                                                                                                                                                                                                                                  _STRPY
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01-AUG-1988
01-AUG-1988
16-OCT-2001
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
-!- FUNCTION: Involved in DNA double-strand break repai
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between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00470; RecF; SMART; SM00382; AAA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
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InterPro; IPR001687;
InterPro; IPR001238;
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                 NCBI_TaxID=1314;
                                                                  Bacteria; Firmicutes;
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                                                                                                                                      protein,
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SUBUNIT: Forms a complex with mrell (By similarity).
SIMILARITY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rad50/mre11 complex possesses single-strand endonuclease activated and ATP-dependent double-strand-specific exonuclease activity Rad50 provides an ATP-dependent control of mre11 by unwinding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and/or repositioning DNA ends into the mrell active site
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(Rel.
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144
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precursor.
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21.9%;
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Recf.
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ATP (BY SIMILARITY).
COILED COIL (POTENTIAL)
3970 MW; FDB177EC7E026479 CRC
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annotation
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Pred. No. 0.18;
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  (See http://www.isb-sib.ch/announce/
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                                                               group;
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                                                                                                                                                                                                                                                                                                                                                                                                                        314
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                                                               Streptococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0015; GPOSANCHOR.
PROSITE; PS00343; GRAM_POS_ANCHORING;
                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                           Coiled coil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00746; Gram_pos_anchor; 1.
Pfam; PF02370; M; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                       DOMAIN
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InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR003345; M_repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M11338; AAA26920.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=85166224;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
              220
                                                                165
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                                                                                                                                                              55 KRTIINKLFFDLAQEEENVLDREFLKNELDNVRAQLSQKDK--EKRDSQVIIDTLRDTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tt J.R., Pulliam W.M., Hollingshead S.K., Fischetti V.A.;
lationship of M protein genes in group A streptococci.";
c. Natl. Acad. Sci. U.S.A. 82:1822-1826(1985).
FUNCTION: THIS PROTEIN IS ONE OF THE DIFFERENT ANTIGENIC SEROTYPES
OF PROTEIN M. PROTEIN M IS CLOSELY ASSOCIATED MITH VIRULENCE OF
THE BACTERIUM AND CAN RENDER THE ORGANISM RESISTANT TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Type I membrane p
SIMILARITY: TO OTHER M PROTEINS.
SIMILARITY: TO OTHER STREPTOCOCCAL AND
IN THE REGION OF THE MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                        KKTLDETVKDKIAKEQESKETIGTLKKTLDE-----TVKDKIAKEQESKETIGTLKKTLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHAGOCYTOSIS.
TMEQIELLLQSQLPEVEE-----MIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASG
                                     ----ELAKKDEGNKVSEASRKGLRRDLDASREAKKQVEKDLANLTAELDKVKEEKQISD
                                                                                        ETVKDKIAKEQ --- ESKETIGTLKKIL -----
                                                                                                                ERNATVVSLQQALGKAEMLCSTLKKQMKYLEQQQDET-----KQAQEEAGRLRSKMK
                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phagocytosis;
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458
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478
157
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483
457
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347
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                                                                                                                                                                                                        6.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell
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                                                                                                                                                                                                      Score 163.5;
Pred. No. 0.1
                                                                                                                                                                                                                                                                                                                                                                        M PROTEIN, SEROTYPE 6.
EXTRACELLULAR (POTENTIAL
MEMBRANE ANCHOR.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                      PROTEINS
                                                                                                                                                                                                                                                                                              HYDROPHILIC.
GLY/PRO-RICH
                                                                                                                                                                                                                                                                                                                        10 X 7 AA TANDEM REPEATS.
4.5 X 25 AA TANDEM REPEATS.
TWO DIRECTLY REPEATED 27 AMINO
BLOCKS SEPARATED BY 15 AMINO AC
                                                                                                                                                                                                                                                                                  CONSERVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                     wall;
                                                                                                                                                                                                                                                            68F87F28DB53A448
                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scott J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat; Antigen;
                                                                                        -DETVKDKIAREQKSKQDIGALKQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           There are no restrictions on it no as its content is in no ved. Usano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M protein of the membrane anchor.
                                                                                                                                                                                                                                                                                  GRAM-POSITIVE
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Y373_BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Trachea;
Jovov B., Ripoll P.J., Benos D.J.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea Bovidae; Boyinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y373_BOVIN
Q9TU23;
                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein; DOMAIN 37 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KIAA0373
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                                                                                                                                                                                                                                                  36 QSFETA-----PSRTCPQCRIQVGKRTIINKLFFDLAQE---
                                                                                                                                                                                                                                                                                              Local
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KIKEFENMKLRLQENHADEVKKIKAEVED-LRCLLVQSQKESQSLKSELQTQKEANSRAP
                           --KEYENLK-----EARKASGEVADKLRKDLFSSRSKLQTVYSEL--------
                                                                                                                                                                                                                          QKFEEATGSMPDPSLPIPN-QLEIALRKIKENIRIILETQATCRSLEEKLREKESALRLA
                                                      ETAWDLIKQSPTPVPTNKHFIRLAEMEQTVAEQDDSLSSLVIKLKQVSQDLERQKEITEL
                                                                                                                                     SLQQALGKAEMLCSTLKKQMKYLEQQQDE----TKQAQEEAGRLRSKMKTMEQ
                                                                                                                                                                                             EENVLDREFLKNEL - - - - - - - - DNVRAQLSQKDKEKRDSQVIIDTLRDTLEERNATVV 119
                                                                               ---IELLLQS--QLPEVEEMIRDMGVGQSAVEQ---LAVYCVSLK----
                                                                                                            NMQARLNQKE---EVLKKYQHLLEKAREEQREIVKKHEEELHTLHRKLELQADNSLSKFK
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                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   requires a license agreement (See http://www.isb-sib.ch/announce/
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AA: 169934 MW;
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5; Mismatches
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Pred. No. 0.35;
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W; 03CBA02A64CF4139 CRC64;
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X MEDLINE-20196006; PubMed=10731132;
X MEDLINE-20196006; PubMed=10731132;
XA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
XA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
XA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
XA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
XA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
XA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
XA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
XA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
XA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
XA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
XA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
XA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DROME
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P15215; Q24373; Q9VT18;
01-APR-1990 (Rel. 14, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Laminin gamma-1 chain precursor (Laminin B2 chain).
LAND2 OR LANC1 OR LANG1 OR CG3322.

Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-CANTON-S. AND OREGON-R;
STRAIN-STRAIN-CANTON-S. AND OREGON-R;
MEDLINE-9129161; PubMed-1840513;
Chi H.-C., Juminaga D., Wang S.Y.,
Chi H.-C., Wang S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Primary structure of the Drosophila laminin B2 chain and comparison with human, mouse, and Drosophila laminin B1 and B2 chains."; J. Biol. Chem. 264:1543\cdot1550(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=OREGON-R;
MEDLINE=89109164; PubMed=2912972;
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"Drosophila laminin: sequence of B2 subunit and expression three subunits during embryogenesis.";
J. Cell Biol. 109:2441-2453(1989).
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RA Durbin K.J., Evangelistat C.C., Ferraz C., Ferriera S., Fleischmann W., RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Ra Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Glodek A., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Liu X., Mattei B., McIntosh T.C., McLedd M.P., McPherson D., RA McIkolov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., RA Mount S.M., Pithman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Sun E., RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., RA Williams S.M., Wooldage T., Worley K.C., Wu D., Yang S., Yao Q.A., RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., RA Zheng X.H., Zhong F.N., Zhong M., Zhong S., Zhu X., Smith H.O., RA Zheng S.H., Zhong F.N., Zhong M., Zhong S., Zhu X., Smith H.O., RA Zheng S.H., Weinstock G.M., Venter J.C.;
RRA Science 287:2185-2195(2000).
RT "CDMA and amino acid sequences of Drosophila laminin B2 chain.";

RI Nucleic Acids Res. 16:7205-7205(1988).

C: FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ C: THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING C: ISTHOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING C: I-- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND TO SUBGUNIT BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.

C: SUBCELLULAR LOCATION: BASEMENT MEMBRANES (MAJOR COMPONENT).

C: SUBCELLULAR LOCATION: BASEMENT MEMBRANES (MAJOR COMPONENT).

C: DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COLLED COIL STRUCTURE.

C: SUMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN VI).

C: SIMILARITY: CONTAINS 1 LAMININ BOG-LIKE DOMAINS.

C: SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
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InterPro; IPR000034; Laminin\_B. InterPro; IPR002049; Laminin\_EGF; Pfam; PF00052; Laminin\_B; 1. pfam; PF00053; Laminin\_EGF; 10. Pfam; PF00055; Laminin\_Nterm; 1. EMBL; M58417; AAA28665.1; -.
EMBL; M25063; AAA28664.1; -.
EMBL; AE003551; AAF50238.1; -.
EMBL; X07806; CAA30665.1; -.
EMBL; X07806; CAA30665.1; -. use by non-profit modified and this st This FlyBase; FBgn0002528; LanB2. InterPro; IPR000561; EGF-like. InterPro; IPR001886; LamNT. or send the European Bioinformatics Institute. The business of the second state of the second entities requires a between HSSP; P02468; SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its s requires a license agreement (S an email to license@isb-sib.ch). PD002082; this statement 1TLE LamNT; 1 .' is not removed. (See http://www.isb-sib as its content and for .ch/announce/ ņ

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PROSITE; PS01248; LA PROSITE; PS01186; EC PROSITE; PS01248; LA Glycoprotein; Baschaminin EGP
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SM00136; LamNT;
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1186; EGF_2; 1.
1248; LAMININ_TYPE_EG; Basement membrane;
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                   ALMI_SCHPO STANDAKU;

C Q9UTK5; O13313; Q9UTT8;

T 16-OCT-2001 (Rel. 40, Created)

T 16-OCT-2001 (Rel. 40, Last sequence update)

JT 16-OCT-2001 (Rel. 40, Last annotation update)

JT 16-OCT-2001 (Rel. 40, Last annotation update)

JE Abnormal long morphology protein 1 (Sp8).

SA ALM1 OR SPAC1486.04C.

OS Schizosaccharomyces pombe (Fission yeast).

OS Schizosaccharomycetales; Schizosaccharomycetes;

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomyceteae;
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STRAIN=972;
STRAIN=972;
MEDLINE=20123449; PubMed=10660053;
Jimenez M., Petit T., Gancedo C., Goday C
"The alml+ gene from Schizosaccharomyces
protein that associates with the medial :
unl Gen. Genet. 262:921-930(2000).
                                                                                                                                     STRAIN-972;
McDougall R.C., Rajandream M.A., Barrell B.G., McDougall R.C. (DEC-1999) to the EMBL/GenBank/DDBJ Submitted (DEC-1999)
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NCBI_TaxID=4896;
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-!- FUNCTION: AFTER THE ONSET OF MITOSIS, AT MID- TO LATE ANAPHASE CO-LOCALIZES WITH THE MEDIAL ACTIN RING. MAY PLAY A ROLE IN
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Interpro; IPR002928; I
Interpro; IPR002017; Interpro; IPR001609; I
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"Human nonmuscle myosin heavy chains are en on different chromosomes.";
Circ. Res. 69:530-539(1991).
-i- FUNCTION: CELLULAR MYOSIN APPEARS TO PL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-96025307; PubMed-7499478;
Phillips C.L., Yamakawa K., Adelstein R.S.;
"Cloning of the cDNA encoding human nonmuscle myosin heavy ch
analysis of human tissues with isoform-specific antibodies.";
J. Muscle Res. Cell Motil. 16:379-389(1995).
                                                                                 Myosin;
Coiled c
DOMAIN
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SMART; SP
PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents
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Mammalia; Eutheria;
                DOMAIN
NP_BIND
MOD_RES
MOD_RES
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HSSP; P08799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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[2]
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                                                                                                                                                                  ProDom;
                                                                                                                                                                              PRINTS;
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CAPPING.

CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC CREGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITUE, CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPT. CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.

SIMILARITY: CONTAINS 1 1Q DOMAIN.
                                                                                                                                                           n; PF00612; IQ; 1.
n; PF00063; myosin_head; 1.
n; PF00736; Myosin_N; 1.
m; PF01576; Myosin_tail; 1.
NTS; PR00193; MYOSINHEAVY.
DDm; PD000355; myosin_head; 1
T; SM00015; TQ; 1.
T; SM00015; TQ; 1.
TE; PS50096; TQ; 1.
T; ATP-binding; Calm,
Coil; Alkylation; b,
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(Rel. 33, Last sequence update)
(Rel. 40, Last annotation update)
// Chain, nonmuscle type B (Cellular myosin heavy chain, record myosin heavy chain-B) (NMMHC-B).
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Chordata; C
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Myosin_N.
Myosin_tail.
Spectrin.
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                                                                                                                                                                                                                                             myosin_head
                                                                                             Multigene
             IQ.
COLLED COIL (POTENTIAL).
ATP (POTENTIAL).
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ALKYLATION (SH-2). (POTEN
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                                                                                   MYOSIN
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                             (POTENTIAL)
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P15924; Q14189; O75993; Q9UHN4;
O1-APR-1990 (Rel. 14, Created)
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   MEDLINE-90153880;
                   TISSUE-Foreskin,
                                   SEQUENCE OF 1120-2871 FROM N.A. (ISOFORM DPI)
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Pfam;
SMART;
SMART;
                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The amino-terminal domain of desmoplakin binds to plakoglobin (clusters desmosomal cadherin-plakoglobin complexes.";
J. Cell Biol. 139:773-784(1997).
-I- FUNCTION: MAJOR HIGH MOLECULAR WEIGHT PROTEIN OF DESMOSOMES
                                                                                                                            PIR; A35536; A35536.
HSSP; P01100; 1FOS.
                                                                                                                                                                                                                                                                 or send
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Dhaliwal A.S., Corcoran C.M., Denning M.F., Green I
"The amino-terminal domain of desmoplakin binds to
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Angst B.D.,
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Angst B.D., Nilles L.A.;
"Structure of the human desmoplakins.
the desmosomal plaque.";
J. Biol. Chem. 265:2603-2612(1990).
                                                                         InterPro;
                                                                                        InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                               DISEASE: DEFECTS IN DSP ARE A CAUSE OF STRIATE PALMOPLANTAR KERATODERMA II (PPKS2, KPPS2 OR SPPK2), CHARACTERIZED BY SKIN THICKENING IN THE PALMS (LINEAR PATTERN) AND THE SOLES (ISLAND-LIKE PATTERN) AND FLEXOR ASPECT OF THE FINGERS; AND RARELY BY ABNORMALITIES OF THE NAILS, THE TEETH AND THE HAIR. SIMILARITY: CONTAINS 17 PLECTIN REPEATS.
SIMILARITY: CONTAINS 2 SPECTRIN REPEATS.
SIMILARITY: BELONGS TO THE PLAKIN OR CYTOLINKER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Invest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBGUNIT: HOMODIMER.
SUBGELLULAR LOCATION: INNERMOST PORTION OF THE DESMOSOMAL PLAQUE.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; DPI/DP1 (SHOWN HERE) AND
DPII/DP2; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: DPI IS APPARENTLY AN OBLIGATE CONSTITUENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALL DESMOSOMES; DPII RESIDE PREDOMINANTLY IN TISSUES AND CELLS OF STRATIFIED ORIGIN.

STRATIFIED ORIGIN.

DOMAIN: THE N-TERMINAL REGION IS REQUIRED FOR LOCALIZATION TO THE DESMOSOMAL PLAQUE AND INTERACTS WITH THE N-TERMINAL REGION OF PLAKOPHILIN 1. THE C-TERMINAL REGION INTERACTS WITH INTERMEDIATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INVOLVED IN THE ORGANIZATION OF THE DESMOSOMAL CADHERIN-
PLAKOGLOBIN COMPLEXES INTO DISCRETE PLASMA MEMBRANE DOMA
THE ANCHORING OF INTERMEDIATE FILAMENTS TO THE DESMOSOME
                                                                                                              125647;
                 PF00681; Plectin_repeat;
; SM00250; PLEC; 17.
; SM00150; SPEC; 1.
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AF139065; AAF19785.1;
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Coiled
                                                                                                                                                                                                                                                                   an email to license@isb-sib.ch)
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IPR002017;
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Nilles L.A.;
em. 265:11406-11407(1990).
coil;
Phosphorylation; Cytoskeleton;
                                                                         Spectrin.
                                                                                          Plectin_repeat
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K.J.;
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P12883; Q14904; Q16579;
O1-OCT-1989 (Rel. 12, Created)
O1-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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Liew C.-C., Sole M.J., Yamauchi-Takihara K.,
Anderson D.H., Lin L., Liew J.;
"Complete sequence and organization of the h
heavy chain gene.";
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Mammalia; Eutheria;
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    characterization
                                       SEQUENCE OF 1393-1935 FROM N.A. MEDLINE=87192738; PubMed=3032769; Jandreski M.A., Liew C.-C.;
                                                                                                                                         myosin
                                                                                                                                                                                                                       TISSUE=Skeletal muscle;
MEDLINE=90235862; PubMed=1691980;
                                                                                                                                                                                                                                                                                                        J. Clin.
                                                                                                                                                                                                                                                                                                                                            expression
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[6]
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"Characterization
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Pfordt M., Bach A., Vosberg H.P.;
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    skeletal muscle.";
    ds Res. 14:2951-2969(1986)
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nem. 189:55-65(1990).
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K., Sole M.J., Liew J., Ing D., Liew
of human cardiac myosin heavy chain c
Sci. U.S.A. 86:3504-3508(1989).
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.A. 86:7416-7417(1989).
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Catarrhini;
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human cardiac alpha- a
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Circulation
                                                                                                                                                                      hypertrophic cardiomyopathy.";
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associated with two distinct mutations in the beta-myosin heavy ch
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                                                                                                                                 VARIANT CMH1 ASN-615
                                                                                                                                                                                                                                      Moolman J.C., Brink P.A., Corfield V.A.; Identification of a new missense mutation
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Genet. 58:267-276(1995).
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629; PubMed=8254035;
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R., Hirayama K.,
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Towbin J., Seidman C.E., Roberts R.:
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VARIANT
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MEDLINE-93343938; Pub
Harada H., Kimura A.,
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Kuan P., Wu C.-W., Lien W.-P., Liew C.-C.;
Walignant familial hypertrophic cardiomyopathy
453Arg-->Cys mutation in the beta-myosin heavy o
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MEDLINE=96047159; Pub
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"A missense mutation of cardiac beta-myosin
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                                               EDQMNEHRSKAEETQRSVNDLTSQRAKLQTENGELSRQLDEKEALI-SQLTRGKLTYTQQ
                                                                                         KKQMKYLEQQQDETKQAQEEAGRLRSKMKT---
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pubmerlain S., Cleland
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RESULT 37

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AC P11538; 013228;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 140, Last sequence updated)
DT 16-CCT-2001 (Rel. 40, Last annotation updated)
DT 16-CCT-2001 (Rel. 4
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Maita T., Miyanishi T., Matsuzono K., Tanioka Y., Matsuda G.;
"The primary structure of skeletal muscle myosin heavy chain:
Sequence of the 22 kDa fragment and the alignment of the 23 kD
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"The primary structure of skeletal muscle myosin heavy chain:
Sequence of the 50 kDa fragment of subfragment-1.";
J. Biochem. 110:60-67(1991).
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ence of the amino-terminal 23 kDa fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T., Yajima E., Nagata S., Miyanishi T., Nakayama S., Matsuda G.; primary structure of skeletal muscle myosin heavy chain: IV. ince of the rod, and the complete 1,938-residue sequence of the
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Aves; Neognathae; Galliformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - VYSELDQAKLELKSAQKDLQSADKEIMSLKKKLTMLQET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Pectoralis muscle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ
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ion update)
e, adult.
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mes; Phasianidae; Phasiani
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motor.";
Science
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F-ACTIN AND HAS ATPASE ACTIVITY THAT IS ACTIVATED BY F-ACTIN.

SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC),

AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,

CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,

CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

-I- PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY
ALKYLATED AND ARE REQULAED FOR MYOSIN CAN BE SPLIT INTO 1 LIGHT
MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete amino-acid sequence skeletal muscle myosin.";
                                                                                                                                                                                                                                      PIR;
PIR;
                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not remove entities requires a license agreement (so or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Embedding of the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-93303624: PubMed-8316857;
Rayment I., Rypniewski W.R., Schm
Tomchick D.R., Benning M.M., Wink
Holden H.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1857-1938
MEDLINE-87217964; Pubm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subfragment
Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Amino-acid sequence of
skeletal muscle myosin."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=89228549;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coung R.B.
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                                                                                                                                   ML; U87231; AAB47555.1;

MIG557; AAA48970.1;

RY PX0050; PX0051.

RY PX0051; A26821.

RY PX0521; A26821.

RY PX0521; A26821.

RY PX04501.

RY PX0450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBFRAGMENT (S2).
SIMILARITY: CONTAINS 1 MYOSIN-LIKE
SIMILARITY: CONTAINS 1 IQ DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261:50-58(1993)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hoppe-Seyler
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1938 FROM N.A. PubMed=3034534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=2713098,
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                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLOBULAR HEAD DOMAIN.
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MBL outstation -
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InterPro; IPR000048; InterPro; IPR004009; InterPro; IPR002928; InterPro; IPR001609; InterPro; IPR001609; Pfam; PF00612; IQ; 2.

; IQ. ; Myosin\_N. ; Myosin\_tail. myosin\_head

myosin\_head; 1.

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RESULT 38

KF4A_HUMAN
ID KF4A_H
AC 095339
DT 15-UTL
DT 16-OCT
DT 16-OCT
DT 16-OCT
DT CTCOMO
GN KIF4A
OS HOMO S
OC Eukary
OC Mammal
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Best Local S
Matches 65
                                                                                           KF4A_HUMAN STANDARD; PRT; 1232 AA. 095239; Q9UMW3; Q9UNY6; Q9UY24; 15-JUL-1999 (Rel. 38, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Chromosome-associated kinesin KIF4A (Chromokinesin).
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CONFLICT

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  Mammalia; Eutheria; NCBI_TaxID=9606;
                                      Homo sapiens (Human).
Eukaryota; Metazoa; C
                                                                               KIF4A OR KIF4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1255
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00015; IQ; 1
SMART; SM00242; MYSC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
PfoDom; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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METHYLATION (TRI-).

METHYLATION (MONO-).

ALKYLATION (SH-1).

ALKYLATION (SH-2).

C -> Q (IN REF. 7 AND 8).

L -> F (IN REF. 1).

E -> D (IN REF. 5).

S -> A (IN REF. 5).

HV -> QL (IN REF. 5).

S -> A (IN REF. 10).

I -> V (IN REF. 10).

IHG -> FH (IN REF. 10).
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ACTIN-BINDING.
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                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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n; Acetylation;
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EMBL; AF071592; AAD5492.2; -.
EMBL; AF271784; CAB75427.1; -.
EMBL; AF277375; AAF86334.1; -.
HSSP; P1711; 3KAR.
InterPro; IPR001752; kinesin.
Pfam; PF00225; kinesin; 1.
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CONFLICT
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Retinoblastoma; Rentsch A., Neumann T., Submitted (FEB-2000) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. TISSUE-Lymphocytes; Villard L.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Retinoblastoma; MEDLINE=97311419; PubMed=9168136;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yan R.-T., Wang S.-Z.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 128-1232 FROM N.A.
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PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
Motor protein; Microtubules; ATP-binding; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     superfamily motor protein.";
Biochim. Biophys. Acta 1493:219-224(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Increased chromokinesin immunoreactivity
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FUNCTION: REQUIRED FOR MITOTIC CHROMOSOMAL POSITIONING AND BIPOI SPINDLE STRABILIZATION (BY SIMILARITY).

SUBCELLULAR LOCATION: NUCLEAR, ASSOCIATED WITH MITOTIC CHROMOSOMES (BY SIMILARITY).

TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEMATOPOIETIC TISSUES, FETAL LIVER, SPLEEN, THYMUS AND ADULT THYMUS AND BONE MARROW. LOVER LEVELS ARE FOUND IN HEART, TESTIS, KIDNEY, COLON AND LUNG. SIMILARITY; BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.

CHROMOKINESIN SUBFAMILY.
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the EMBL/GenBank/DDBJ
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                                                                                                                                                                                        MYS_AEOIR STANDARD; PRT; 1938 & P24733; P24733; Ol-MAR-1992 (Rel. 21, Created) Ol-MAR-1992 (Rel. 21, Last sequence update 16-CCT-2001 (Rel. 40, Last annotation update Myosin heavy chain, striated muscle. Aequipecten irradians (Bay scallop). Eukaryota; Metazoa; Mollusca; Bivalvia; Pt
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                                                                                                                    TISSUE-Adductor muscle; MEDLINE-92011595; PubMed-1917970;
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                                                                       that
                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                     Pectinoidea; Pect
NCBI_TaxID=31199;
                       SEQUENCE FROM N.A.
TISSUE=Adductor muscle;
                                                                                           Nyitray L., Goodwin E.B., Szent-Gyoergyi A.G.; "Complete primary structure of a scallop striated muscle
 MEDLINE=91088319; PubMed=2263488;
Nyitray L., Goodwin E.B., Szent-G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104;
                                                          Sequence comparison with other heavy chains ight be critical for regulation.";
1. Chem. 266:18469-18476(1991).
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-> N (IN REF. 2).
-> S (IN REF. 2).
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InterPro: IPR004009; Myosin_N.
InterPro: IPR002928; Myosin_tail
InterPro: IPR0029217; Spectrin.
InterPro: IPR002017; Spectrin.
InterPro: IPR001609; myosin_head
Pfam; PF00061; IQ; 2.
Pfam; PF00063; myosin_head; 1.
Pfam; PF002736; Myosin_N; 1.
Pfam; PF01776; Myosin_Kail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWI
between
                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
entities requires a license agreement (See http://www.isb
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: MUSCLE CONTRACTION.

-!- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO F-ACTIN & HA ACTIVITY THAT IS ACTIVATED BY F-ACTIN.

-!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSI HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNIT AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

-!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
-!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
-!- SIMILARITY: CONTAINS 1 10 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Szent-Gyorgyi A.G., come. ...
"Structure of the regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Nucleotide sequence of full length cDNA muscle myosin heavy chain."; Nucleic Acids Res. 18:7158-7158(1990).
         TURN
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PIR; S13557; S13557.
PIR; A40997; A40997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xie X., Harrison D.H.,
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"Structure of the regulatory
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                                                                                                                                                                                            ; SM00015; IQ; 1.
; SM00242; MYSC; 1
; FS50096; IQ; 1
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                                                                                                                                                                                  protein;
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Myosin_tail.
Spectrin.
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MYOSIN HEAD-LIKE.
                                                                        RODLIKE TAIL (S2 AND LMM COILED COIL (POTENTIAL).
ATP (BY SIMILARITY).
ALKYLATION (SH-1) (BY SIM ALKYLATION (SH-2) (BY SIM
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                                                                          (BY SIMILARITY).
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Query Match Best Local Similarity

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Submitted
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99996; Q9UQQ4; Q9UQQ4; Q9UQQ4; Q9Y6Y2; Q14869; Q43355; Q94895; Q9Y6B8;

16-QCT-2001 (Rel. 40, Created)

16-QCT-2001 (Rel. 40, Last sequence update)

16-QCT-2001 (Rel. 40, Last annotation update)

A-kinase anchor protein 9 (Protein kinase A anchoring protein 9)

(PRKA9) (A-kinase anchor protein 450 KDa) (AKAP 450) (A-kinase anchor protein 450 KDa) (AKAP 120 like protein)

(Hyperion protein) (Yotiao protein) (Centrosome- and golgi-localized PKN-associated protein) (CG-NAP).

AKAP9 OR AKAP450 OR AKAP350 OR KIAA0803.
                                                                                                                                                                                 MEDLINE=99287934; PubMed=10358086;
Takahashi M., Shibata H., Shimakawa M., Miyamoto M., Mu
"Characterization of a novel giant scaffolding protein,
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   SEQUENCE OF
                                                        "Cloning of Hyperion
                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                apparatus
                                                                                                                                                                  anchors multiple signaling
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                             Witczak O., Skaalhegg B.S., Keryer Jahnsen T., Oerstavik S.; "Cloning and characterization of a protein located in the centrosome,
                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-99219864;
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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"Yotiao, a
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                                                                                                                                                                                                                                                                                              18:1858-1868(1999)
                                                                                                                                                                                                                                                                                                                                                                                                          FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wyszynski M., Madhavan R., Sealock R., Kim J.U., Sheng I a novel protein of neuromuscular junction and brain that with specific splice variants of NMDA receptor subunit
                                         (AUG-1998)
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                                                                                                                               274:17267-17274(1999).
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                                                                                                                                                                                                                                                                                                                                                                              PubMed=10202149;
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                                                                                                                                                                                                                                                            (ISOFORM
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                                       EMBL/GenBank/DDBJ databases
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in, CG-NAP,
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                                                                                                                                                                                   Ono Y.;
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   SEQUENCE OF 17-1800 FROM N.A.

WU X., GRAVES T., Bradshaw H.;
SUBMITTED (SEP-1998) to the EMBL/Genbank/DDBJ databases.

SUBMITTED (SEP-1998) TO TYPE II REGULATORY SUBUNITS OF PROTEIN KINASE AND FROTEIN SINDS TO TYPE II REGULATORY SUBUNITS OF PROTEIN KINASE AND PHOSPHATASES ON CENTROSOME AND GOLGI APPARATUS WHERE PHYSIOLOGICAL EVENTS CAN BE REGULATED BY PHOSPHORYLATION STATE OF PROTEIN SUBSTRATES. ISOFORM 4/YOTIAO IS ASSOCIATED WITH THE N-METHYL-D-ASPARTATE RECEPTOR AND IS SPECIFICALLY FOUND IN THE NEUROMUSCULAR JUNCTION (NMJ) AS WELL AS IN NEURONAL SYNAPSES EXPLAINING THAT ITS ROLE MAY BE TO ORGANIZE POSTSYNAPTIC SPECIALIZATIONS.

-I- SUBUNIT: INTERACTS WITH THE REGULATORY REGION OF PROTEIN KINASE N (PKN), PROTEIN PHOSPHATASE 2A (PP2A), PROTEIN PHOSPHATASE 1 (PP1) AND THE IMMATURE NON-PHOSPHORYLATED FORM OF PKC EPSILON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schmidt P.H., Dransfield D.T., Claudio J.O., Trotter K.W., Milgram S.L., Goldenring J.R.; "AKAP350, a multiply spliced protein kinase /
                                     EMBL;
                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XI The complete sequences of 100 new cDNA clones from brain which code
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Lung;
Milgram S.L., Goldenr
"AKAP350: A multiply
association.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Lymphoblast;
Hinds K., Sutterer C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "AKAP350, a multiply spliced protein associated with centrosomes.";
                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed
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                                                         EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN-1998) to
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MEDLINE=99115654; PubMed=9915845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol.
                                                                                                                                                                                                                                                                     EXPRESSED IN SKELETAL MUSCLE AND IN PANCREAS.

DOMAIN: RII BINDING SITE, PREDICTED TO FORM AMPHIPATHIC COULD PARTICIPATE IN PROTEIN-PROTEIN INTERACTIONS WITH A COMPLEMENTARY SURFACE ON THE R-SUBUNIT DIMER.

CAUTION: REF. 6 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO TWO FRAMESHIFTS IN POSITIONS 3782 AND 3811.

CAUTION: REF. 9 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FOUR FRAMESHIFTS IN POSITIONS 39, 1653, 1699 AND 1735.
                                                                                                                                                                                                                                                                                                                                                                                                                                      NAP, 4/YO
SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SÜBCELLULAR LOCATION: CENTROSOMAL IN MANY CELL TYPES CYTOPLASMIC IN PARLETAL CELLS.
ALTERNATIVE PRODUCTS: 6 ISOFORMS; 1 (SHOWN HERE), 2, NAP, 4/YOTIAO, 5 AND 6/AKAP350; ARE PRODUCED BY ALTEI
                                                                                                                                                                                                    European
                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE
                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                       AJ131693;
AB019691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  large proteins in vitro.";
Res. 5:277-286(1998).
AJ010770;
AF026245;
AF083037;
AC004013;
                                                                                                                             an
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                                                                                                                               email to
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                                                                                                                                                                                   Bioinformatics Institute. The profit institutions as long
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CAB40713.1;
BAA78718.1;
CAA09361.1;
AAB86384.1;
AAD22767.1;
AAB968667.1;
                                                                                                                               license@isb-sib.ch).
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                                                                                                                                                . Usage by and for commercial
http://www.isb-sib.ch/announce/
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; BAA34523.1;
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PKA-RII SUBUNIT BINDING DOMAIN.
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COILED COIL (POTENTIA
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E -> Q (IN REF. 3)
M -> I (IN REF. 3)
E -> G (IN REF. 3)
E -> N (IN REF. 3)
H -> N (IN REF. 3)
H -> N (IN REF. 3)
H -> N (IN REF. 1)
O -> P (IN REF. 3)
O -> H (IN REF. 3)
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                                                                  Score 162.5; I
Pred. No. 1.2;
                                               Mismatches
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V (IN REF. 3).

N (IN REF. 8).

N (IN REF. 8).

D (IN REF. 3).

D (IN REF. 3).

H (IN REF. 3).

H (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                                                    TVVSLQQALGKAEMLCSTLKKQMKYLEQQ----QDETKQAQEEAGRLRSKMKTMEQIELL
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                                                             VLFGKFAQIIQEKEVEIDQLNEQVTK----LQQQLKITTDNKVIEEKNELIRDLETQIECL
                                                                                            GYYEKLC--LEKSHSPIQDVPKKICKGPRKESQLSLGGQSCAGEPDEELVGAFPIFVRNA
                                                                                                                             -NKNEEVQQLHMQLEIQKKESTTRLQ-ELEQENKLFKDDME-KLGLAIKESDAMSTQDQH
                                                                                                                                                           PVASETVDRLVL-----ESPAPVEVNLKLRRPSFRDDIDLNATFDVDTPPARPSSSQH
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                                                                                                                                                                                                                                                           SEHQTREVEQLANHLKEKTDKCSELLLSKEQLQRDIQERNEEIEKLEFRVRE-LEQALLV
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Search completed: September 4, 2002, 16:17:19
Job time: 478 sec

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